

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 13, 2003, 20:42:19 ; Search time 25 Seconds  
(without alignments)  
40.855 Million cell updates/sec

Title: US-09-939-293a-19\_COPY\_56\_62  
Perfect score: 33  
Sequence: 1 AVPIAK 7

Scoring table: BLOSOM62  
Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues  
Total number of hits satisfying chosen parameters: 32153

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA.\*  
1: /cgn2\_6/ptodata/2/pubppa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppa/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppa/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppa/PCTUS\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppa/US08\_NEW\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubppa/US09\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubppa/US09A\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubppa/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubppa/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/2/pubppa/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubppa/US10A\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubppa/US10B\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubppa/US10C\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubppa/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/2/pubppa/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubppa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	33	100.0	7	10 US-09-939-293-6	Sequence 6, Appl1
2	33	100.0	7	10 US-09-965-967-8	Sequence 8, Appl1
3	33	100.0	7	12 US-10-293-371-1	Sequence 1, Appl1
4	33	100.0	7	12 US-10-293-371-24	Sequence 24, Appl1
5	33	100.0	7	12 US-10-293-371-45	Sequence 45, Appl1
6	33	100.0	7	14 US-10-068-569-12	Sequence 12, Appl1
7	23	69.7	5	10 US-09-939-293-5	Sequence 5, Appl1
8	23	69.7	5	14 US-10-068-569-20	Sequence 20, Appl1
9	23	69.7	5	14 US-10-068-569-24	Sequence 24, Appl1
10	23	69.7	5	15 US-10-197-634-2	Sequence 2, Appl1
11	22	66.7	7	12 US-10-293-371-27	Sequence 27, Appl1
12	22	66.7	7	12 US-10-293-371-35	Sequence 35, Appl1
13	22	66.7	7	12 US-10-293-371-38	Sequence 38, Appl1
14	22	66.7	7	12 US-10-293-371-39	Sequence 39, Appl1
15	22	66.7	7	12 US-10-293-371-51	Sequence 51, Appl1

16	20	60.6	7	16 US-10-305-346-8	Sequence 8, Appl1
17	19	57.6	4	10 US-09-939-293-13	Sequence 13, Appl1
18	19	57.6	4	10 US-09-965-967-1	Sequence 1, Appl1
19	19	57.6	4	12 US-10-293-371-76	Sequence 76, Appl1
20	19	57.6	4	14 US-10-068-569-21	Sequence 21, Appl1
21	19	57.6	7	12 US-10-293-371-20	Sequence 20, Appl1
22	18	54.5	6	10 US-09-818-656A-20	Sequence 20, Appl1
23	18	54.5	7	9 US-09-924-889-5	Sequence 5, Appl1
24	18	54.5	7	10 US-09-884-767A-125	Sequence 125, App
25	18	54.5	7	11 US-09-753-139C-4	Sequence 4, Appl1
26	18	54.5	7	11 US-09-753-139C-5	Sequence 5, Appl1
27	18	54.5	7	12 US-10-293-371-9	Sequence 9, Appl1
28	18	54.5	7	12 US-10-293-371-33	Sequence 33, Appl1
29	18	54.5	7	12 US-10-014-322A-82	Sequence 82, Appl1
30	17	51.5	5	14 US-10-014-485A-127	Sequence 127, App
31	17	51.5	5	15 US-10-288-966-12	Sequence 12, Appl1
32	17	51.5	6	10 US-09-777-921A-16	Sequence 16, Appl1
33	17	51.5	7	9 US-09-096-749A-32	Sequence 32, Appl1
34	17	51.5	7	11 US-09-903-412-32	Sequence 32, Appl1
35	17	51.5	7	11 US-09-851-486-96	Sequence 96, Appl1
36	17	51.5	7	12 US-10-165-155-32	Sequence 32, Appl1
37	17	51.5	7	12 US-10-286-457-108	Sequence 108, App
38	17	51.5	7	15 US-10-174-717A-32	Sequence 32, Appl1
39	17	51.5	7	15 US-10-128-966-37	Sequence 37, Appl1
40	16	48.5	4	10 US-09-947-387-46	Sequence 46, Appl1
41	16	48.5	4	15 US-10-100-957A-84	Sequence 84, Appl1
42	16	48.5	5	14 US-10-014-485A-123	Sequence 123, Appl1
43	16	48.5	7	10 US-09-801-042-12	Sequence 12, Appl1
44	16	48.5	7	12 US-09-777-656A-3	Sequence 3, Appl1
45	16	48.5	7	12 US-09-777-656A-4	Sequence 4, Appl1

## ALIGNMENTS

RESULT 1  
US-09-939-293-6  
; Sequence 6, Application US/09939293  
; Patent No. US20020132786A1  
; GENERAL INFORMATION:  
; APPLICANT: Alnemerl, Emad S.  
; TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE  
; FILE REFERENCE: 480140.465  
; CURRENT APPLICATION NUMBER: US/09/939,293  
; CURRENT FILING DATE: 2001-08-24  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 6  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-939-293-6

Query Match 100.0%; Score 33; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVPIAK 7  
Db 1 AVPIAK 7  
RESULT 2  
US-09-965-967-8  
; Sequence 8, Application US/09965967  
; Patent No. US2002017757A1  
; GENERAL INFORMATION:  
; APPLICANT: Shi, Yigong  
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis  
; FILE REFERENCE: PU-0031 (01-1739-1)  
; CURRENT APPLICATION NUMBER: US/09/965,967  
; CURRENT FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: 60/236,574  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/256,830  
; PRIOR FILING DATE: 2000-12-20  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-965-967-8

Query Match 100.0%; Score 33; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVPIAOK 7  
Db 1 AVPIAOK 7

RESULT 3  
US-10-293-371-1  
; Sequence 1, Application US/10293371  
; Publication No. US20030157522A1  
; GENERAL INFORMATION:  
; APPLICANT: BOUDREAU, ALAIN  
; APPLICANT: KORNELOK, ROBERT G.  
; APPLICANT: LACASSE, ERIC  
; APPLICANT: LISTON, PETER  
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
; TITLE OF INVENTION: Interaction Screens  
; FILE REFERENCE: 07891/030002  
; CURRENT APPLICATION NUMBER: US/10/293,371  
; PRIOR FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: US 60/370,934  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: US 60/332,300  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-10-293-371-1

Query Match 100.0%; Score 33; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVPIAOK 7  
Db 1 AVPIAOK 7

RESULT 4  
US-10-293-371-24  
; Sequence 24, Application US/10293371  
; Publication No. US20030157522A1  
; GENERAL INFORMATION:  
; APPLICANT: BOUDREAU, ALAIN  
; APPLICANT: KORNELOK, ROBERT G.  
; APPLICANT: LACASSE, ERIC  
; APPLICANT: LISTON, PETER  
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
; TITLE OF INVENTION: Interaction Screens  
; FILE REFERENCE: 07891/030002  
; CURRENT APPLICATION NUMBER: US/10/293,371  
; CURRENT FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: US 60/370,934

; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: US 60/332,300  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-10-293-371-24

Query Match 100.0%; Score 33; DB 12; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVPIAOK 7  
Db 1 AVPIAOK 7

RESULT 5  
US-10-293-371-45  
; Sequence 45, Application US/10293371  
; Publication No. US20030157522A1  
; GENERAL INFORMATION:  
; APPLICANT: BOUDREAU, ALAIN  
; APPLICANT: KORNELOK, ROBERT G.  
; APPLICANT: LACASSE, ERIC  
; APPLICANT: LISTON, PETER  
; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
; TITLE OF INVENTION: Interaction Screens  
; FILE REFERENCE: 07891/030002  
; CURRENT APPLICATION NUMBER: US/10/293,371  
; PRIOR FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: US 60/370,934  
; PRIOR FILING DATE: 2002-04-08  
; PRIOR APPLICATION NUMBER: US 60/332,300  
; PRIOR FILING DATE: 2001-11-09  
; NUMBER OF SEQ ID NOS: 85  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
; US-10-293-371-45

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Best Local Similarity 100.0%; Pred. No. 4.8e+05;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVPIAOK 7  
Db 1 AVPIAOK 7

RESULT 6  
US-10-068-569-12  
; Sequence 12, Application US/10068569  
; Publication No. US20020160975A1  
; GENERAL INFORMATION:  
; APPLICANT: Srinivasula, Srinivasa M.  
; APPLICANT: Fernandes-Alnemri, Teresa  
; APPLICANT: Alnemri, Emdad S.  
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN  
; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS  
; FILE REFERENCE: 480140.475  
; CURRENT APPLICATION NUMBER: US/10/068,569  
; CURRENT FILING DATE: 2002-02-06  
; NUMBER OF SEQ ID NOS: 28

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-12
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AVPIA 7
Db 1 AVPIA 7
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RESULT 7
US-09-939-293-5
; Sequence 5, Application US/09939293
; Patent No. US20020132786A1
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; GENERAL INFORMATION:
; APPLICANT: Alnemrl, Emad S.
; TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
; FILE REFERENCE: 480140.465
; CURRENT APPLICATION NUMBER: US/09/939,293
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-293-5
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Query Match
Best Local Similarity 100.0%; Score 23; DB 10; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AVPIA 5
Db 1 AVPIA 5
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RESULT 8
US-10-068-569-20
; Sequence 20, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemrl, Teresa
; APPLICANT: Alnemrl, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-20
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Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AVPIA 5
Db 1 AVPIA 5
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RESULT 9
US-10-068-569-24
; Sequence 24, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemrl, Teresa
; APPLICANT: Alnemrl, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-24
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Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AVPIA 5
Db 1 AVPIA 5
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US-10-197-634-2
; Sequence 2, Application US/10197634
; Publication No. US20030073629A1
; GENERAL INFORMATION:
; APPLICANT: Alnemrl, Emad S.
; TITLE OF INVENTION: OMI AND DOMAINS THEREOF THAT DISRUPT
; TITLE OF INVENTION: IAP-CASPASE INTERACTION
; FILE REFERENCE: 480140.479
; CURRENT APPLICATION NUMBER: US/10/197,634
; CURRENT FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-197-634-2
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AVPIA 5
Db 1 AVPIA 5
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RESULT 11
US-10-293-371-27
; Sequence 27, Application US/10293371
; Publication No. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAULT, ALAIN
; APPLICANT: KORNEJUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-B1r
; TITLE OF INVENTION: Interaction Screens
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
```

;; PRIOR APPLICATION NUMBER: US 60/370,934  
;; PRIOR FILING DATE: 2002-04-08  
;; PRIOR APPLICATION NUMBER: US 60/332,300  
;; PRIOR FILING DATE: 2001-11-09  
;; NUMBER OF SEQ ID NOS: 85  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 27  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic  
US-10-293-371-27

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVPIA 5  
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Db 1 AIPPIA 5

RESULT 12  
US-10-293-371-35  
;; Sequence 35, Application US/10293371  
;; Publication No. US20030157522A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BOUDREAU, ALAIN  
;; APPLICANT: KORNEILUK, ROBERT G.  
;; APPLICANT: LACASSE, ERIC  
;; APPLICANT: LISTON, PETER  
;; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
;; FILE REFERENCE: 07891/030002  
;; CURRENT APPLICATION NUMBER: US/10/293,371  
;; CURRENT FILING DATE: 2003-04-08  
;; PRIOR APPLICATION NUMBER: US 60/370,934  
;; PRIOR FILING DATE: 2002-04-08  
;; PRIOR APPLICATION NUMBER: US 60/332,300  
;; PRIOR FILING DATE: 2001-11-09  
;; NUMBER OF SEQ ID NOS: 85  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 35  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic  
US-10-293-371-35

Query Match  
Best Local Similarity 66.7%; Score 22; DB 12; Length 7;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVPIA 5  
1:||||  
Db 1 AIPPIA 5

RESULT 13  
US-10-293-371-38  
;; Sequence 38, Application US/10293371  
;; Publication No. US20030157522A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BOUDREAU, ALAIN  
;; APPLICANT: KORNEILUK, ROBERT G.  
;; APPLICANT: LACASSE, ERIC  
;; APPLICANT: LISTON, PETER  
;; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
;; FILE REFERENCE: 07891/030002  
;; CURRENT APPLICATION NUMBER: US/10/293,371

;; CURRENT FILING DATE: 2003-04-08  
;; PRIOR APPLICATION NUMBER: US 60/370,934  
;; PRIOR FILING DATE: 2002-04-08  
;; PRIOR APPLICATION NUMBER: US 60/332,300  
;; PRIOR FILING DATE: 2001-11-09  
;; NUMBER OF SEQ ID NOS: 85  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 38  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic  
US-10-293-371-38

Query Match  
Best Local Similarity 66.7%; Score 22; DB 12; Length 7;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVPIA 5  
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Db 1 AIPPIA 5

RESULT 14  
US-10-293-371-39  
;; Sequence 39, Application US/10293371  
;; Publication No. US20030157522A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BOUDREAU, ALAIN  
;; APPLICANT: KORNEILUK, ROBERT G.  
;; APPLICANT: LACASSE, ERIC  
;; APPLICANT: LISTON, PETER  
;; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
;; FILE REFERENCE: 07891/030002  
;; CURRENT APPLICATION NUMBER: US/10/293,371  
;; CURRENT FILING DATE: 2003-04-08  
;; PRIOR APPLICATION NUMBER: US 60/370,934  
;; PRIOR FILING DATE: 2002-04-08  
;; PRIOR APPLICATION NUMBER: US 60/332,300  
;; PRIOR FILING DATE: 2001-11-09  
;; NUMBER OF SEQ ID NOS: 85  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 39  
;; LENGTH: 7  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Synthetic  
US-10-293-371-39

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Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVPIA 5  
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Db 1 AIPPIA 5

RESULT 15  
US-10-293-371-51  
;; Sequence 51, Application US/10293371  
;; Publication No. US20030157522A1  
;; GENERAL INFORMATION:  
;; APPLICANT: BOUDREAU, ALAIN  
;; APPLICANT: KORNEILUK, ROBERT G.  
;; APPLICANT: LACASSE, ERIC  
;; APPLICANT: LISTON, PETER  
;; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir  
;; FILE REFERENCE: 07891/030002

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; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-51
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Best Local Similarity 80.0%; Pred. No. 4.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY      1 AVPIA 5
        |:| | |
Db      1 AVPIA 5
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Search completed: September 13, 2003, 20:47:12  
Job time : 26 secs

THIS PAGE RI ANK

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 13, 2003, 20:41:40 ; Search time 80 Seconds  
(without alignments)  
13.889 Million cell updates/sec

Title: US-09-939-293a-19\_COPY\_56\_62  
Perfect score: 33  
Sequence: 1 AVPIAOK 7

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 76613

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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8: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1986.DAT: \*  
9: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1987.DAT: \*  
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13: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1991.DAT: \*  
14: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1992.DAT: \*  
15: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1993.DAT: \*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	7	23	ABB76213 Human smac (DIABLO)
2	33	100.0	7	23	AAU78434 Inhibitor of apopt
3	33	100.0	7	23	AAU78487 Smac-7 AV peptid.
4	28	84.8	6	23	ABB76214 Human smac (DIABLO)
5	28	84.8	6	23	AAU78486 Smac-6 AV peptid.
6	23	69.7	5	23	ABB76215 Human smac (DIABLO)
7	23	69.7	5	23	AAU78433 Inhibitor of apopt
8	23	69.7	5	23	AAU78485 Smac-5 AV peptid.
9	23	69.7	5	24	ABF71308 Smac IAP-binding m

10	21	63.6	6	20	AAV14088 Affinity ligand fo
11	21	63.6	7	23	AAU78488 Smac-7R AV peptid
12	21	60.6	7	7	AAPE1490 Angiotensin conver
13	20	60.6	7	14	AAAR30536 ACE inhibiting pep
14	20	60.6	7	15	AAAR37103 Bovine milk beta-c
15	20	60.6	7	24	ABJ37331 G-protein coupled
16	20	60.6	7	24	ABJ37411 G-protein coupled
17	19	57.6	4	23	ABB76220 Human smac (DIABLO)
18	19	57.6	4	23	AAU97413 Human Smac (second
19	19	57.6	4	23	AAU78441 Inhibitor of apopt
20	19	57.6	4	23	AAU78484 Smac-4 AV peptid.
21	19	57.6	7	23	ABB98612 Dextrane-sacchara
22	18	54.5	4	23	AAE29600 Metallopeptide C-t
23	18	54.5	4	23	ABG32329 P. vivax circumspo
24	18	54.5	5	12	AAAR12732 Pentapeptide paral
25	18	54.5	5	16	AAAR69964 Pentameric mimoto
26	18	54.5	5	17	AAAR98710 Control peptide fo
27	18	54.5	5	21	AAV99478 Plant acyltransfer
28	18	54.5	5	21	AAV52447 Rat GLUT4-eGFP fus
29	18	54.5	6	15	AAAR58328 Hypotensive polype
30	18	54.5	6	21	AAAB12611 Halovir B peptide
31	18	54.5	6	23	AAAE29605 Metallopeptide C-t
32	18	54.5	6	24	ABU13773 Novel human transp
33	18	54.5	7	14	AAAR39444 Crystalline trypti
34	18	54.5	7	15	AAAR58327 Hypotensive polype
35	18	54.5	7	20	AAAY50563 Insulin production
36	18	54.5	7	23	AAAE29595 Metallopeptide #14
37	18	54.5	7	23	AAAE29609 Metallopeptide C-t
38	18	54.5	7	23	AAPE2608 CXC chemokine rece
39	18	54.5	7	23	ABB83463 Tissue inhibitor o
40	18	54.5	7	23	ABB83464 Tissue inhibitor o
41	18	54.5	7	23	AAO14001 Cysteine-X-Cystein
42	18	54.5	7	23	AAU81658 Enterokinase recog
43	17	51.5	5	24	ABU64702 Motif-specific and
44	17	51.5	6	21	AAAB35910 Peptide conveying
45	17	51.5	6	22	AAAB49754 Complex sugar boun

#### ALIGNMENTS

RESULT 1	ABB76213	standard; Peptide; 7 AA.
ID	ABB76213	
XX	ABB76213:	
AC	09-AUG-2002	(first entry)
XX		
DT	Human smac (DIABLO) derived peptide.	
XX		
DE	DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;	
KW	human; cancer; cyclostatic; mutant; muten.	
KM		
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	7
FT		/note- "optional C-terminal protecting group,
FT		e.g. C-terminal amide"
XX		
PN	WO200230959-A2.	
PD	18-APR-2002.	
XX		
PF	12-OCT-2001; 2001MO-US32121.	
XX		
PR	13-OCT-2000; 2000US-0687549.	
XX		
PA	(ABBO ) ABBOTT LAB.	
XX		
PI	Fesik SW, Meadows RP, Betz SP, Liu Z, Olejniczak ET, Sun C;	
XX		

DR WPI: 2002-444169/47.  
XX  
XX Novel peptide derived from wild-type human second mitochondria derived  
PT activator of caspase protein useful for identifying candidate  
PT substances to kill cancerous cells  
XX  
XX  
PS Claim 5; Page 7; 26pp; English.  
XX  
CC The present sequence is a peptide derived from wild-type human  
CC second mitochondria derived activator of caspase (smac), also known  
CC as direct inhibitor of apoptosis binding protein with low pI  
CC (DIABLO). The peptide is one of 12 claimed smac (DIABLO)-derived  
CC peptides (see ABB76208-19) which bind to the Bir2 and Bir3 domain  
CC of XIAP, an inhibitor of apoptosis protein (IAP) family member.  
CC Kd values for Bir-3 and Bir-2 are 0.70 +/- 0.09 uM and 9.4 +/- 0.6  
CC uM, respectively, for the present (C-terminally amidated) peptide,  
CC compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively,  
CC for full-length smac. Modification of the N-terminal alanine  
CC destroys binding affinity to XIAP, and mutation of the valine,  
CC proline or isoleucine also causes some loss of binding. Amino  
CC acids C-terminal to the isoleucine are not important for binding.  
CC The claimed peptides can be used to identify candidate substances  
CC which induce or promote apoptosis in cells. The assay involves  
CC determination of the ability of candidate compounds to disrupt the  
CC binding interaction between a smac (DIABLO) peptide and an IAP  
CC family member.  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 33; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVPIAQK 7  
DB 1 AVPIAQK 7  
RESULT 2  
AAU78434  
ID AAU78434 standard; Peptide: 7 AA.  
XX  
XX AAU78434;  
XX  
XX 18-JUN-2002 (first entry)  
XX  
DE Inhibitor of apoptosis (IAP) protein Smac, mutant Smac-N7.  
XX  
XX Human; Inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2;  
XX Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy;  
XX neoplastic cell; mutant; tumour.  
XX  
XX Homo sapiens.  
XX Synthetic.  
XX  
XX WO200216418-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 24-AUG-2001; 2001WO-US26492.  
XX  
XX 24-AUG-2000; 2000US-227735P.  
XX  
XX (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
XX Alnemr1 ES;  
XX  
XX WPI: 2002-304115/34.  
XX  
XX Novel Smac peptides and polynucleotides encoding the peptides, useful  
XX for stimulating apoptosis in neoplastic or tumour cell which  
XX overexpresses inhibitor of caspase, and for identifying apoptosis  
XX modulating compounds

XX  
XX Example 3; Fig 7; 76pp; English.  
XX  
XX The invention relates to an isolated smac peptide or polypeptide (I)  
CC and an isolated nucleic acid (II) encoding (I). Also described is a  
CC method of identifying a compound that inhibits apoptosis, comprising:  
CC (a) separately contacting several cell populations expressing a  
CC cytosolic Smac (a Smac isoform that begins with MKSDRF sequence,  
CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)),  
CC and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting  
CC domain) with a compound to be tested for apoptotic inhibiting activity;  
CC (b) incubating the cell populations with a direct stimulus of the cell  
CC death pathway; and (c) measuring the specific apoptotic activity of the  
CC cell populations, where inhibition of the specific apoptotic activity is  
CC indicative that the compound is an inhibitor of apoptosis. (I) and (II)  
CC are useful for inducing apoptosis in a cell. The Smac polypeptide and  
CC polynucleotide are useful for stimulating apoptosis in a neoplastic or  
CC tumour cell which overexpresses an inhibitor of caspase, where the  
CC inhibitor inhibits activation or activity of caspase-3, caspase-7 or  
CC caspase-9. Preferably, the cell overexpresses at least a portion of IAP.  
CC (I) is useful for identifying an inhibitor or enhancer of a caspase-  
CC mediated apoptosis which involves contacting a cell transformed or  
CC transfected with a vector expressing (I) with a candidate inhibitor or  
CC candidate enhancer; and detecting cell viability, where an increase in  
CC cell viability indicates the presence of an inhibitor and a decrease in  
CC cell viability indicates the presence of an enhancer. Optionally, the  
CC method involves detecting the presence of large and small caspase  
CC subunits after contacting cell transformed with the vector expressing  
CC (I), with the candidate compound. A decrease in processing indicates the  
CC presence of an inhibitor and an increase in the processing indicates the  
CC presence of an enhancer. Preferably, the large and small subunits of  
CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for  
CC identifying a compound that inhibits Smac binding to Smac-binding  
CC molecule (a portion of IAP e.g. a BIR domain such as BIR1, BIR2 or BIR3,  
CC or a full-length IAP). (II) is useful in gene therapy techniques. The  
CC present sequence represents the amino acid sequence of Smac mutant  
CC Smac-N7.  
XX  
SQ Sequence 7 AA;  
Query Match 100.0%; Score 33; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVPIAQK 7  
DB 1 AVPIAQK 7  
RESULT 3  
AAU78487  
ID AAU78487 standard; Peptide: 7 AA.  
XX  
XX AAU78487;  
XX  
XX 18-JUN-2002 (first entry)  
XX  
XX Smac-7 AV peptoid.  
XX  
XX Apoptosis; cytosolic; apoptotic; AV peptoid; melanoma; lymphoma;  
XX Inhibitor of Apoptosis protein; IAP; procaspase-3; tumour cell;  
XX breast cancer; prostate cancer; lung cancer; pancreatic cancer; smac-7;  
XX gastric cancer; colon cancer; ovarian cancer; renal cancer; hepatoma;  
XX sarcoma; smac; second mitochondria-derived activator of caspases.  
XX  
XX Synthetic.  
XX  
XX WO200216402-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 23-AUG-2001; 2001WO-US41869.  
XX



PA 23-AUG-2000; 2000US-0645075.  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PI Wang X, Du C;  
XX WPI; 2002-280909/32.  
XX  
XX  
XX Composition for enhancing the apoptosis of pathogenic cells,  
PT particularly tumour cells, e.g. breast cancer, prostate cancer, lung  
PT cancer, colon cancer, ovarian cancer or sarcoma, comprises apoptotic  
PT compounds -  
XX  
XX Example 9; Page 28; 40pp; English.  
XX  
XX This invention relates to a method for induction of apoptosis in  
CC pathogenic cells. The method comprises a novel pharmaceutical  
CC composition which comprises an AV peptoid in dosage form and a  
CC pharmaceutical carrier, where the AV peptoid comprises a peptide that  
CC interacts with or inhibits the activity of an inhibitor of Apoptosis  
CC protein (IAP) as measured by IAP binding, procaspase-3 activation or  
CC promotion of apoptosis. The peptoids of the invention are used to  
CC inhibit an inhibitor of Apoptosis protein (IAP). Compositions containing  
CC these peptide are useful for enhancing the apoptosis of pathogenic  
CC cells, particularly tumour cells, e.g. breast cancer, prostate cancer,  
CC lung cancer, pancreatic cancer, gastric cancer, colon cancer, ovarian  
CC cancer, renal cancer, hepatoma, melanoma, lymphoma or sarcoma. The  
CC composition is particularly useful for promoting cell death. The  
CC present sequence represents an AV peptoid (smac-7) used to inhibit  
CC second mitochondria-derived activator of caspases (smac) using the  
CC method of the invention. Smac interacts with and eliminates the activity  
CC of a number of IAP's and as such inhibiting its activity allows the  
CC induction of apoptosis.  
CC  
SQ Sequence 7 AA;  
  
Query Match 100.0%; Score 33; DB 23; Length 7;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AVPIAQ 7  
DB 1 AVPIAQ 7  
  
RESULT 4  
AB76214  
ID AB76214 standard; Peptide; 6 AA.  
XX  
AC AB76214;  
XX  
XX 09-AUG-2002 (first entry)  
XX  
XX Human smac (DIABLO) derived peptide.  
DE  
XX  
XX DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;  
KW human; cancer; cytostatic; mutant; mutleln.  
KW  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 6 /note="optional C-terminal protecting group,  
FT /note="e.g. C-terminal amide"  
XX  
XX WO200230959-A2.  
XX  
XX 18-APR-2002.  
XX  
XX 12-OCT-2001; 2001WO-US32121.  
XX  
XX 13-OCT-2000; 2000US-0687549.  
XX

PA (ABBO ) ABBOTT LAB.  
XX  
XX Resik SW, Meadows RP, Betz SP, Liu Z, Olejniczak ET, Sun C;  
XX WPI; 2002-444169/47.  
XX  
XX  
XX Novel peptide derived from wild-type human second mitochondria derived  
PT activator of caspase protein useful for identifying candidate  
PT substances to kill cancerous cells -  
XX  
XX Claim 5; Page 7; 26pp; English.  
XX  
XX  
XX The present sequence is a peptide derived from wild-type human  
CC second mitochondria derived activator of caspase (smac), also known  
CC as direct inhibitor of apoptosis binding protein with low PI  
CC (DIABLO). The peptide is one of 12 claimed smac (DIABLO)-derived  
CC peptides (see AB76208-19) which bind to the Bir2 and Bir3 domain  
CC of XIAP, an inhibitor of apoptosis protein (IAP) family member.  
CC Kd values for Bir-3 and Bir-2 are 0.80 +/- 0.2 uM and 8.9 +/- 0.6  
CC uM, respectively, for the present (C-terminally amidated) peptide,  
CC compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively,  
CC for full-length smac. Modification of the N-terminal alanine  
CC destroys binding affinity to XIAP, and mutation of the valine,  
CC proline or isoleucine also causes some loss of binding. Amino  
CC acids C-terminal to the isoleucine are not important for binding.  
CC The claimed peptides can be used to identify candidate substances  
CC which induce or promote apoptosis in cells. The assay involves  
CC determination of the ability of candidate compounds to disrupt the  
CC binding interaction between a smac (DIABLO) peptide and an IAP  
CC family member.  
XX  
SQ Sequence 6 AA;  
  
Query Match 84.8%; Score 28; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AVPIAQ 6  
DB 1 AVPIAQ 6  
  
RESULT 5  
AAU78486  
ID AAU78486 standard; Peptide; 6 AA.  
XX  
AC AAU78486;  
XX  
XX 18-JUN-2002 (first entry)  
XX  
XX Smac-6 AV peptoid.  
DE  
XX  
XX Apoptosis; cytostatic; apoptotic; AV peptoid; melanoma; lymphoma;  
KW inhibitor of Apoptosis protein; IAP; procaspase-3; tumour cell;  
KW breast cancer; prostate cancer; lung cancer; pancreatic cancer; smac-6;  
KW gastric cancer; colon cancer; ovarian cancer; renal cancer; hepatoma;  
KW sarcoma; smac; second mitochondria-derived activator of caspases.  
KW  
XX  
OS Synthetic.  
XX  
XX WO200216402-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 23-AUG-2001; 2001WO-US41869.  
XX  
XX 23-AUG-2000; 2000US-0645075.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Wang X, Du C;  
XX  
XX WPI; 2002-280909/32.  
XX

XX Composition for enhancing the apoptosis of pathogenic cells,  
PT particularly tumour cells, e.g. breast cancer, prostate cancer, lung  
PT cancer, colon cancer, ovarian cancer or sarcoma, comprises apoptotic  
PT compounds -  
PS  
XX  
PS Example 9; Page 28; 40pp; English.  
XX  
CC This invention relates to a method for induction of apoptosis in  
CC pathogenic cells. The method comprises a novel pharmaceutical  
CC composition which comprises an AV peptide in dosage form and a  
CC pharmaceutical carrier, where the AV peptide comprises a peptide that  
CC interacts with or inhibits the activity of an inhibitor of apoptosis  
CC protein (IAP) as measured by IAP binding, procaspase-3 activation or  
CC promotion of apoptosis. The peptides of the invention are used to  
CC inhibit an inhibitor of Apoptosis protein (IAP). Compositions containing  
CC these peptides are useful for enhancing the apoptosis of pathogenic  
CC cells, particularly tumour cells, e.g. breast cancer, prostate cancer,  
CC lung cancer, pancreatic cancer, gastric cancer, colon cancer, ovarian  
CC cancer, renal cancer, hepatoma, melanoma, lymphoma or sarcoma. The  
CC composition is particularly useful for promoting cell death. The  
CC present sequence represents an AV peptide (smac-6) used to inhibit  
CC second mitochondria-derived activator of caspases (smac) using the  
CC method of the invention. Smac interacts with and eliminates the activity  
CC of a number of IAP's and as such inhibiting its activity allows the  
CC induction of apoptosis.  
CC  
XX  
SQ Sequence 6 AA;  
Query Match 84.8%; Score 28; DB 23; Length 6;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVPIAQ 6  
DB 1 AVPIAQ 6  
RESULT 6  
ABR76215  
ID ABR76215 standard; Peptide; 5 AA.  
XX  
AC ABR76215;  
XX  
DT 09-AUG-2002 (first entry)  
XX  
DE Human smac (DIABLO) derived peptide.  
XX  
KW DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;  
KW human; cancer; cytostatic; mutant; mutain.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Modified-site 5 /note="optional C-terminal protecting group,  
FT e.g. C-terminal amide"  
XX  
XX WO200230959-A2.  
XX  
XX 18-APR-2002.  
XX  
XX 12-OCT-2001; 2001WO-US32121.  
XX  
XX 13-OCT-2000; 2000US-0687549.  
XX  
XX (ABB0 ) ABBOTT LAB.  
XX  
XX Fesik SW, Meadows RP, Betz SP, Liu Z, Olejniczak ET, Sun C;  
XX  
XX WPI; 2002-444169/47.  
XX  
PT Novel peptide derived from wild-type human second mitochondria derived

PT activator of caspase protein useful for identifying candidate  
PT substances to kill cancerous cells -  
PS  
XX  
PS Claim 5; Page 7; 26pp; English.  
XX  
CC The present sequence is a peptide derived from wild-type human  
CC second mitochondria derived activator of caspase (smac), also known  
CC as direct inhibitor of apoptosis binding protein with low pI  
CC (DIABLO). The peptide is one of 12 claimed smac (DIABLO)-derived  
CC peptides (see ABR76208-19) which bind to the Bir2 and Bir3 domain  
CC of XIAP, an inhibitor of apoptosis protein (IAP) family member.  
CC Kd values for Bir-3 and Bir-2 are 0.64 +/- 0.07 uM and 5.5 +/- 0.5  
CC uM, respectively, for the present (C-terminally amidated) peptide,  
CC compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively,  
CC for full-length smac, showing that a peptide of 5 amino acids  
CC retained full binding affinity to the Bir3 domain of XIAP.  
CC Modification of the N-terminal alanine destroyed binding affinity  
CC to XIAP, and mutation of the valine, proline or isoleucine also  
CC caused some loss of binding. The claimed peptides can be used to  
CC identify candidate substances which induce or promote apoptosis in  
CC cells. The assay involves determination of the ability of  
CC candidate compounds to disrupt the binding interaction between a  
CC smac (DIABLO) peptide and an IAP family member.  
CC  
XX  
SQ Sequence 5 AA;  
Query Match 69.7%; Score 23; DB 23; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVPIA 5  
DB 1 AVPIA 5  
RESULT 7  
AAU78433  
ID AAU78433 standard; Peptide; 5 AA.  
XX  
AC AAU78433;  
XX  
DT 18-JUN-2002 (first entry)  
XX  
DE Inhibitor of apoptosis (IAP) protein Smac, long isoform peptide.  
XX  
KW Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; Bir1; Bir2;  
KW Bcl2 interacting domain; caspase; Bir domain; Bir3; gene therapy;  
KW neoplastic cell; tumour.  
XX  
OS Homo sapiens.  
XX  
XX WO200216418-A2.  
XX  
XX 28-FEB-2002.  
XX  
XX 24-AUG-2001; 2001WO-US26492.  
XX  
XX 24-AUG-2000; 2000US-227735P.  
XX  
XX (UYJE-) UNIV JEFFERSON THOMAS.  
XX  
XX Alnemri ES;  
XX  
XX WPI; 2002-304115/34.  
XX  
XX  
XX Novel smac peptides and polynucleotides encoding the peptides, useful  
XX for stimulating apoptosis in neoplastic or tumour cell which  
XX overexpresses inhibitor of caspase, and for identifying apoptosis  
XX modulating compounds -  
XX  
XX Example 5; Fig 12; 78pp; English.  
XX  
XX The invention relates to an isolated smac peptide or polypeptide (I)



PT apoptosis proteins, useful for regulating or altering caspase-mediated  
PT apoptosis and for treating cancer, tumor, or autoimmune diseases -  
PS Example 1; Page 44; 83pp; English.  
XX  
XX The invention relates to polynucleotides encoding an Omi (serine  
CC protease) peptide or polypeptide. The Omi peptide specifically binds to a  
CC portion of an inhibitor of Apoptosis Protein (IAP). The Omi polypeptide  
CC induces caspase-independent apoptosis, or fails to have serine protease  
CC activity. The Omi peptides are useful for regulating or altering  
CC apoptosis, specifically caspase-mediated apoptosis, and as immunogens for  
CC raising antibodies. Enhancers of apoptosis are useful for treating  
CC cancers, tumours or for destroying cells that mediate autoimmune  
CC diseases. Compositions may also be used for the treatment of diseases  
CC associated with inappropriate activation of apoptosis such as  
CC neurodegenerative diseases and ischemic injury. The antibodies can be  
CC used in isolating Omi peptides, polypeptides and their variants, in  
CC identifying molecules that interact with Omi peptides and polypeptides,  
CC and in inhibiting or enhancing the biological activity of Omi peptides  
CC and polypeptides. The present sequence represents a Smac IAP-binding  
CC motif peptide.  
XX  
SQ Sequence 5 AA:  
Query Match 69.7%; Score 23; DB 24; Length 5;  
Best Local Similarity 100.0%; Pred. No. 9.3e+05;  
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVPIA 5  
DB 1 AVPIA 5  
RESULT 10  
AA114088  
ID AA114088 standard; peptide; 6 AA.  
XX  
XX AA114088;  
AC  
XX  
XX 21-JUL-1999 (first entry)  
DT  
XX  
XX Affinity ligand for Hba1c.  
DE  
XX  
XX Affinity ligand; Hba1c; glycosylated haemoglobin; biosensor production;  
KW  
XX sensor system; multiple organ damage; diabetes.  
OS  
XX Synthetic.  
XX  
XX WO921015-A2.  
PN  
XX  
XX 29-APR-1999.  
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XX 21-OCT-1998; 98WO-GB03148.  
PF  
XX  
XX 08-JUL-1998; 98GB-0014670.  
PR  
XX 21-OCT-1997; 97GB-0022116.  
PR 13-MAY-1998; 98GB-0010253.  
XX  
XX (UYCR-) UNIV CRANFIELD.  
PA  
XX  
XX Bestetti G, Chen B, Day R, Turner APF;  
PI  
XX  
XX WPI; 1999-326603/27.  
DR  
XX  
XX Production of affinity ligands useful for measurement of  
PT glycosylated haemoglobin  
PT  
XX  
XX Claim 9; Page 18; 30pp; English.  
PS  
XX  
XX This sequence represents an affinity ligand for the glycosylated  
CC haemoglobin product Hba1c. The invention relates to a method for  
CC providing an affinity ligand which selectively binds to (A) in the  
CC presence of (B) having substantial homology with (A), comprises:

CC (a) generating a combinatorial library of peptides, each different  
CC peptide being bound to a respective separate or separable support member;  
CC (b) screening the library with (B) and separating out any peptides  
CC binding (B) to leave a residual library; and (c) screening the residual  
CC library with (A) and separating out any peptides binding (A), the  
CC peptide(s) constituting one or more of the affinity ligands. The ligands  
CC can be used to produce biosensors and sensor systems, based on the  
CC binding of a ligand to its target causing changes in optical properties  
CC or changes in electrochemical properties. This is particularly useful for  
CC measurement of Hba1c, a glycosylated haemoglobin that initiates and  
CC participates in multiple organ damage that occurs in patients with  
CC diabetes.  
XX  
SQ Sequence 6 AA:  
Query Match 63.6%; Score 21; DB 20; Length 6;  
Best Local Similarity 66.7%; Pred. No. 9.3e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AVPIAO 6  
DB 1 AVFAAE 6  
RESULT 11  
AAU78488  
ID AAU78488 standard; Peptide; 7 AA.  
XX  
XX AAU78488;  
AC  
XX  
XX 18-JUN-2002 (first entry)  
DT  
XX  
XX Smac-7R AV peptoid.  
DE  
XX  
XX Apoptosis; cytosolic; apoptotic; AV peptoid; melanoma; lymphoma;  
KW Inhibitor of Apoptosis protein; IAP; procaspase-3; tumour cell;  
KW breast cancer; prostate cancer; lung cancer; pancreatic cancer; smac-7R;  
KW gastric cancer; colon cancer; ovarian cancer; renal cancer; hepatoma;  
KW sarcoma; smac; second mitochondria-derived activator of caspases.  
XX  
XX Synthetic.  
XX  
XX WO200216402-A2.  
PN  
XX  
XX 28-FEB-2002.  
PD  
XX  
XX 23-AUG-2001; 2001WO-US41869.  
PF  
XX  
XX 23-AUG-2000; 2000US-0645075.  
PR  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
PA  
XX  
XX Wang X, Du C;  
PI  
XX  
XX WPI; 2002-280909/32.  
DR  
XX  
XX Composition for enhancing the apoptosis of pathogenic cells,  
PT particularly tumour cells, e.g. breast cancer, prostate cancer, lung  
PT cancer, colon cancer, ovarian cancer or sarcoma, comprises apoptotic  
PT compounds -  
PT  
XX  
XX Example 9; Page 28; 40pp; English.  
PS  
XX  
XX This invention relates to a method for induction of apoptosis in  
CC pathogenic cells. The method comprises a novel pharmaceutical  
CC composition which comprises an AV peptoid in dosage form and a  
CC pharmaceutical carrier, where the AV peptoid comprises a peptide that  
CC interacts with or inhibits the activity of an inhibitor of Apoptosis  
CC protein (IAP) as measured by IAP binding, procaspase-3 activation or  
CC promotion of apoptosis. The peptoides of the invention are used to  
CC inhibit an inhibitor of Apoptosis protein (IAP). Compositions containing  
CC these peptoids are useful for enhancing the apoptosis of pathogenic  
CC cells, particularly tumour cells, e.g. breast cancer, prostate cancer,

CC lung cancer, pancreatic cancer, gastric cancer, colon cancer, ovarian  
CC cancer, renal cancer, hepatoma, melanoma, lymphoma or sarcoma. The  
CC composition is particularly useful for promoting cell death. The  
CC present sequence represents an AV peptide (smac-7R) used to inhibit  
CC second mitochondria-derived activator of caspases (smac) using the  
CC method of the invention. Smac interacts with and eliminates the activity  
CC of a number of IAP's and as such inhibiting its activity allows the  
CC induction of apoptosis.  
XX  
SQ Sequence 7 AA;  
Query Match 63.6%; Score 21; DB 23; Length 7;  
Best Local Similarity 60.0%; Pred. No. 9.3e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVPIA 5  
| : | : |  
Db 3 AVPIA 7  
RESULT 12  
AAP61490  
ID AAP61490 standard; peptide; 7 AA.  
XX  
AC AAP61490;  
XX  
DT 25-MAR-2003 (updated)  
DT 10-MAR-2003 (updated)  
DT 18-JUL-1991 (first entry)  
XX  
DE Angiotensin converting enzyme inhibitor.  
XX  
KM hypotensive peptide.  
XX  
OS Bos taurus.  
OS Synthetic.  
XX  
PN JPE1036226-A.  
XX  
PD 20-FEB-1986.  
XX  
PF 28-JUL-1984; 84JP-0158324.  
XX  
PR 28-JUL-1984; 84JP-0158324.  
XX  
PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.  
XX  
DR WPI; 1986-090774/14.  
XX  
PT New angiotensin converting enzyme inhibitor - having hypotensive  
PT activity with low side effects.  
XX  
PS Claim 1; Page 187; 4pp: Japanese.  
XX  
CC Inhibitor has hypotensive activity with minimal side effects, it may  
CC be simply prepared from bovine caesin.  
CC (Updated on 10-MAR-2003 to add missing OS field.)  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 7 AA;  
Query Match 60.6%; Score 20; DB 7; Length 7;  
Best Local Similarity 57.1%; Pred. No. 9.3e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AVPIAOK 7  
| | | | :  
Db 1 AVPIAOK 7  
RESULT 13  
AAR30536  
ID AAR30536 standard; peptide; 7 AA.

XX  
XX AAR30536;  
AC  
XX 07-MAY-1993 (first entry)  
DT  
XX  
XX ACE inhibiting peptide #3.  
DE  
XX  
XX angiotensin converting enzyme inhibitor; vasodepressor activity;  
KW low blood pressure; high blood pressure; hypertension; hypotension;  
KW hypertensive; hypotensive.  
XX  
OS Synthetic.  
XX  
PN JP04341193-A.  
XX  
PD 27-NOV-1992.  
XX  
PF 14-MAY-1991; 91JP-0139772.  
XX  
PR 14-MAY-1991; 91JP-0139772.  
XX  
PA (KANE ) KANEBO LTD.  
XX  
DR WPI; 1993-013419/02.  
XX  
XX Prodn. of angiotensin converting enzyme inhibiting peptide - by  
PT sepg. and purifying enzyme decomposition prod. of casein using  
PT ion exchange and hydrophobic resins  
XX  
PS Claim 1; Page 1; 7pp: Japanese.  
XX  
XX This angiotensin converting enzyme (ACE) inhibitor is derived by a  
CC novel method of Prodn. This comprises separation of an enzyme digest  
CC of casein (milk-derived) and purification by ion exchange resin and  
CC hydrophobic resin.  
XX  
SQ Sequence 7 AA;  
Query Match 60.6%; Score 20; DB 14; Length 7;  
Best Local Similarity 57.1%; Pred. No. 9.3e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AVPIAOK 7  
| | | | :  
Db 1 AVPIAOK 7  
RESULT 14  
AAR37103  
ID AAR37103 standard; peptide; 7 AA.  
XX  
AC AAR37103;  
XX  
XX 21-MAY-1995 (first entry)  
DT  
XX  
DE Bovine milk beta-casein enzymatic fragment.  
XX  
KW Beta-casein; enzymatic hydrolysate; cosmetics; skin disorders;  
KW wrinkles.  
XX  
OS Bos Taurus.  
XX  
PN JP06166615-A.  
XX  
PD 14-JUN-1994.  
XX  
PF 01-DEC-1992; 92JP-0321624.  
XX  
PR 01-DEC-1992; 92JP-0321624.  
XX  
PA (POK ) POLA CHEM IND INC.  
XX  
DR WPI; 1994-230615/28.

```

XX  Cosmetics for treating skin disorders and wrinkles - containing
PT  enzymatic hydrolysate of human or bovine milk beta-casein
XX
XX  Claim 2; Page 2; 7pp; Japanese.
PS
XX
CC  The invention relates to cosmetics containing human or bovine milk
CC  beta-casein enzymatic hydrolysate. The cosmetics are used for
CC  improving skin disorders and/or wrinkles. They are more effective
CC  than previously used polysaccharides, sugar alcohols, glycerol,
CC  glycols, etc.
CC  The present sequence is one component of the bovine milk beta-casein
CC  enzymatic hydrolysate.
XX
SQ  Sequence 7 AA:

Query Match      60.6%; Score 20; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY  1 AVPIAQK 7
    ||| |
    1 AVYPPQR 7
DB

```

```

SQ  Sequence 7 AA:

Query Match      60.6%; Score 20; DB 24; Length 7;
Best Local Similarity 66.7%; Pred. No. 9.3e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 VPIAQK 7
    || |
    2 VPFIQK 7
DB

Search completed: September 13, 2003, 20:43:39
Job time : 81 secs

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```

RESULT 15
ABJ37331
ID  ABJ37331 standard; Peptide; 7 AA.
XX
XX  ABJ37331;
AC
XX
XX  08-MAY-2003 (first entry)
DT
XX
DE  G-protein coupled receptor peptide region #43.
XX
XX  Compound library; microenvironment; G-protein Coupled Receptor; GPCR.
XX
XX  Unidentified.
OS
XX  WO2003004147-A2.
PN
XX  16-JAN-2003.
PD
XX  05-JUL-2002; 2002WO-GB03094.
PF
XX  06-JUL-2001; 2001GB-0016570.
PR
XX
XX  (BIOF-) BIOFOCUS PLC.
PA
XX
XX  Crossley R, Rose VS, Stevens AP;
PI
XX  WPI; 2003-221549/21.
DR
XX
XX  Producing compound library, by generating biological target model using
PT  target sequence information, defining microenvironments interacting
PT  with ligand and motifs interacting with microenvironment, and
PT  assembling motifs -
XX
XX  Disclosure; Fig 3; 39pp; English.
PS
XX
CC  The invention relates to a novel method for producing a compound library.
CC  The novel method involves reducing a biological target into a group of
CC  one or more amino acids required for interaction with a ligand, to
CC  generate a model of the biological target, using the model to define a
CC  microenvironment in the biological target capable of interacting with the
CC  ligand, defining motifs which interact with the microenvironment, and
CC  assembling the motifs to generate a compound library for synthesis. The
CC  novel method is useful to produce compound libraries for screening
CC  natural ligands such as peptides and proteins or for producing chemical
CC  compounds based on drug motifs for screening. This sequence represents a
CC  peptide of a G-protein Coupled Receptor (GPCR), which relates to the
CC  novel compound library production method of the invention.
XX

```

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OM protein - protein search, using sw model

Run on: September 13, 2003, 20:41:40 ; Search time 38 Seconds  
(without alignments)  
17.715 Million cell updates/sec

Title: US-09-939-293a-19\_COPY\_56\_62

Perfect score: 33

Sequence: 1 AVPIAK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 456

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	42.4	5	2	E60274
2	13	39.4	5	2	JN0860
3	13	39.4	6	2	A61140
4	13	39.4	7	2	ECMOCR
5	12	36.4	5	2	A60521
6	12	36.4	5	2	S11127
7	12	36.4	6	2	A37765
8	12	36.4	7	2	S66442
9	11	33.3	4	2	I54357
10	11	33.3	5	2	B22565
11	11	33.3	5	2	B37988
12	11	33.3	5	2	US0319
13	11	33.3	6	2	A61049
14	11	33.3	6	2	PQ0008
15	11	33.3	6	2	B60110
16	11	33.3	6	2	I65546
17	11	33.3	7	2	B61491
18	11	33.3	7	2	PM0150
19	11	33.3	7	2	S42620
20	11	33.3	7	2	A39690
21	10	30.3	3	3	E37196
22	10	30.3	3	3	F37196
23	10	30.3	4	2	E44823
24	10	30.3	5	2	JN0862
25	10	30.3	5	2	PQ0009
26	10	30.3	5	2	G37196
27	10	30.3	7	2	A61081
28	10	30.3	7	2	PS0254
29	10	30.3	7	2	I46868

30	9	27.3	4	2	A32039	tyrosine-melanocyte
31	9	27.3	4	2	PT0534	T-cell receptor be
32	9	27.3	5	2	PT0659	T-cell receptor be
33	9	27.3	6	2	A44916	mosquitocidal toxin
34	9	27.3	6	2	PC4127	hypothetical 6 pro
35	9	27.3	6	2	A35039	hypothetical colla
36	9	27.3	6	4	S15596	orf 3 rara 5'-regl
37	9	27.3	7	2	S19630	ribosomal protein
38	9	27.3	7	2	PQ0727	H2 class I protein
39	9	27.3	7	2	S71299	ICL2 protein - Par
40	9	27.3	7	2	A28340	myomodulin - Calli
41	9	27.3	7	2	S09027	carboxylesterase (
42	9	27.3	7	2	PT0269	Ig heavy chain CRD
43	9	27.3	7	2	I48105	dihydrofolate redu
44	9	27.3	7	2	I48086	DNA topoisomerase
45	9	27.3	7	2	PH0932	T-cell receptor be

## ALIGNMENTS

RESULT 1  
E60274  
major protein antigen MP763 - Mycobacterium tuberculosis (fragment)  
C:Species: Mycobacterium tuberculosis  
C:Date: 11-Dec-1992 #sequence\_rev1510n 11-Dec-1992 #text\_change 30-Sep-1993  
C:Accession: E60274  
R:Nagel, S.; Wiker, H.G.; Harboe, M.; Kinomoto, M.  
Infect. Immun. 59, 372-382, 1991  
A:Title: Isolation and partial characterization of major protein antigens in the cult  
A:Reference number: A60274; MUID:9109989; PMID:1898899  
A:Accession: E60274  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <NAC>

Query Match 42.4%; Score 14; DB 2; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVPI 4  
DB 1 AVPI 4

RESULT 2  
JN0860  
peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito  
C:Species: Sarda orientalis (striped bonito)  
C:Date: 10-Mar-1994 #sequence\_rev1510n 10-Mar-1994 #text\_change 07-May-1999  
C:Accession: JN0860  
R:Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory  
A:Reference number: JN0859; MUID:94080036; PMID:7764272  
A:Accession: JN0860  
A:Molecule type: protein  
A:Residues: 1-5 <MAT>  
A:Experimental source: intestine  
C:Comment: The carboxyl-terminus is essential for the protein's expression of angioten  
C:Superfamily: bradykinin-potentiating peptide  
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 39.4%; Score 13; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVPIA 5  
DB 1 ALPHA 5

RESULT 3

A61140  
Sperm acrosomal protein - spoonworm (Urechis caupo) (fragment)  
C:Species: Urechis caupo  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-Apr-1994  
C:Accession: A61140  
R:Gould, M.C.; Stephano, J.L.  
Dev. Biol. 146, 508-518, 1991  
A:Title: Peptides from sperm acrosomal protein that initiate egg development.  
A:Reference number: A61140; MUID:91323672; PMID:1864468  
A:Accession: A61140  
A:Molecule type: protein  
A:Residues: 1-6 <GOU>  
  
Query Match  
Best Local Similarity 39.4%; Score 13; DB 2; Length 6;  
Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 IAKK 7  
Db 1 VAKK 4  
  
RESULT 4  
ECMUCR  
catch-relaxing peptide - blue mussel  
N:Alternate names: CARP  
C:Species: Mytilus edulis (blue mussel)  
C:Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 20-Jun-2000  
C:Accession: A29342  
R:Hirata, T.; Kubota, I.; Takahatake, I.; Kawahara, A.; Shimamoto, N.; Muneoka, Y.  
Brain Res. 422, 374-376, 1987  
A:Title: Catch-relaxing peptide isolated from Mytilus pedal ganglia.  
A:Reference number: A29342; MUID:88052022; PMID:3676797  
A:Accession: A29342  
A:Molecule type: protein  
A:Residues: 1-7 <HIR>  
C:Comment: This peptide exhibits both potentiating (contraction) and inhibitory (relaxat  
C:Superfamily: unassigned animal peptides  
C:Keywords: amidated carboxyl end; hormone; retractor muscle  
F:7/Modified site: amidated carboxyl end (Leu) #status experimental  
  
Query Match  
Best Local Similarity 39.4%; Score 13; DB 2; Length 7;  
Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AVPI 4  
Db 1 AMPM 4  
  
RESULT 5  
A60521  
glycogen phosphorylase (PG 2.4.1.1), muscle - mullet (Liza ramada) (fragment)  
N:Alternate names: glycogen phosphorylase b  
C:Species: Liza ramada  
C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 11-May-2000  
C:Accession: A60521  
R:Bonamura, L.; Baanante, I.V.  
Comp. Biochem. Physiol. B 95, 295-301, 1990  
A:Title: Purification and characterization of glycogen phosphorylase B from skeletal mus  
A:Reference number: A60521; MUID:90227907; PMID:2109669  
A:Accession: A60521  
A:Molecule type: protein  
A:Residues: 1-5 <BON>  
C:Superfamily: glycogen phosphorylase  
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein  
F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim  
  
Query Match  
Best Local Similarity 36.4%; Score 12; DB 2; Length 5;  
Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AVP 3

Db 3 SVP 5  
  
RESULT 6  
S1127  
phosphoprotein, bone - chicken (fragment)  
C:Species: Gallus gallus (chicken)  
C:Date: 21-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 04-Mar-2000  
C:Accession: S1127; S1128  
R:Mikuni-Takagaki, Y.; Glimcher, M.J.  
Biochem. J. 268, 585-591, 1990  
A:Title: Post-translational processing of chicken bone phosphoproteins. Identificatio  
A:Reference number: S1127; MUID:90303246; PMID:2363696  
A:Accession: S1127  
A:Molecule type: protein  
A:Status: preliminary  
A:Residues: 1-5 <MIK1>  
A:Accession: S1128  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 'X', 2-5 <MIK2>  
C:Keywords: phosphoprotein  
  
Query Match  
Best Local Similarity 36.4%; Score 12; DB 2; Length 5;  
Pred. No. 2.8e+05;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 PIAO 6  
Db 2 PVSK 5  
  
RESULT 7  
A3765  
hypothetical protein (csma 5' region) - Chloroflexus aurantiacus (fragment)  
C:Species: Chloroflexus aurantiacus  
C:Date: 31-May-1991 #sequence\_revision 31-May-1991 #text\_change 30-Sep-1993  
C:Accession: A37765  
R:Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.  
J. Bacteriol. 172, 4497-4504, 1990  
A:Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus aurantia  
A:Reference number: A37765; MUID:90330558; PMID:2376566  
A:Accession: A37765  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-6 <THE>  
A:Cross-references: GB:M33964  
  
Query Match  
Best Local Similarity 36.4%; Score 12; DB 2; Length 6;  
Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
  
QY 4 IAKK 7  
Db 3 MAOR 6  
  
RESULT 8  
S66442  
glutathione S-transferase P - rat (fragment)  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 15-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 13-Mar-1997  
C:Accession: S66442  
R:Nishihira, J.; Sakai, M.; Nishi, S.; Hatanaka, Y.  
Eur. J. Biochem. 232, 106-110, 1995  
A:Title: Identification of the electrophilic substrate-binding site of glutathione S-  
A:Reference number: S66442; MUID:96046035; PMID:7556138  
A:Accession: S66442  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-7 <NIS>



Query Match 36.4%; Score 12; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVP 3  
DB 1 ALP 3

RESULT 9

154357  
Schwannomin - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: 154357  
R:Huyh, D.P.; Nechiporuk, T.; Pulst, S.  
Hum. Mol. Genet. 3, 1075-1079, 1994  
A:Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are co  
A:Reference number: 154357; MUID:95072570; PMID:781675  
A:Accession: 154357  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-4 <RES>  
A:Cross-references: GB:U28838; NID:9454836; PIDN:AAA57150.1; PID:9601923  
C:Genetics:  
A:Gene: NF2

Query Match 33.3%; Score 11; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3  
DB 1 VP 2

RESULT 10

B22565  
R-phycoerythrin alpha-2 chain - red alga (Gastrocionium coulteri) (fragment)  
C:Species: Gastrocionium coulteri  
C:Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
C:Accession: B22565  
R:Klotz, A.V.; Glazer, A.N.  
J. Biol. Chem. 260, 4856-4863, 1985  
A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
A:Reference number: A22565; MUID:85182601; PMID:3886644  
A:Accession: B22565  
A:Molecule type: protein  
A:Residues: 1-5 <KID>

Query Match 33.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3  
DB 3 VP 4

RESULT 11

B37988  
acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)  
C:Species: Physarum polycephalum  
C:Date: 28-Jun-1991 #sequence\_revision 28-Jun-1991 #text\_change 30-Sep-1993  
C:Accession: B37988  
R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-Og  
J. Biol. Chem. 265, 19898-19903, 1990  
A:Title: Purification and characterization of a novel intracellular acid proteinase from  
A:Reference number: A37988; MUID:91060608; PMID:2246266  
A:Accession: B37988  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-5 <MDR>

Query Match 33.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PI 4  
DB 4 PI 5

RESULT 12

JS0319  
subesophageal ganglion pentapeptide - house cricket  
C:Species: Acheta domestica (house cricket)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 20-Jun-2000  
C:Accession: JS0319  
R:Wicker, C.; Wicker, C.  
Comp. Biochem. Physiol. C 88, 185-187, 1987  
A:Title: Isolation and structure of a peptide isolated from the subesophageal gangli  
A:Reference number: JS0319  
A:Accession: JS0319  
A:Molecule type: protein  
A:Residues: 1-5 <MIC>

Query Match 33.3%; Score 11; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVP 3  
DB 2 AAP 4

RESULT 13

A61049  
halo-toxin - Pseudomonas syringae pv. mori  
C:Species: Pseudomonas syringae pv. mori  
A:Note: host mulberry tree  
C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 21-Jan-1997  
C:Accession: A61049  
R:Kajimoto, T.; Yokozaki, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata,  
Chem. Lett. 00, 679-680, 1989  
A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas s  
A:Reference number: A61049  
A:Accession: A61049  
A:Molecule type: protein  
A:Residues: 1-6 <KAJ>  
A:Note: sequence confirmed by synthesis  
C:Comment: This toxin is one of the etiological agents of halo bright disease in mulb  
C:Keywords: toxin

Query Match 33.3%; Score 11; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PI 4  
DB 5 PI 6

RESULT 14

PQ0008  
angiotensin-converting enzyme inhibitor (FLP-1) - common fig  
N:Alternate names: ficus latex peptide 1  
C:Species: Ficus carica (common fig)  
C:Date: 07-Jun-1990 #sequence\_revision 07-Jun-1990 #text\_change 08-Dec-1995  
C:Accession: PQ0008  
R:Maruyama, S.; Miyoshi, S.; Tanaka, H.  
Agric. Biol. Chem. 53, 2763-2767, 1989  
A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.  
A:Reference number: PQ0008  
A:Accession: PQ0008  
A:Molecule type: protein

A:Residues: 1-6 <MAR>  
A:Experimental source: latex  
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 33.3%; Score 11; DB 2; Length 6;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PI 4  
II  
Db 4 PI 5

## RESULT 15

B60110  
repetitive protein antigen 61 - Trypanosoma cruzi (fragment)  
C:Species: Trypanosoma cruzi  
C:Date: 10-Nov-1992 #sequence\_revision 10-Nov-1992 #text\_change 18-Jun-1993  
C:Accession: B60110  
R:Hof, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.E.  
Infect. Immun. 57, 1959-1967, 1989  
A:Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.  
A:Reference number: A60110; MUID:89277508; PMID:2659529  
A:Accession: B60110  
A:Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-6 <HOF>  
A:Note: this is an example of a five residue tandem repeat from this protein; the actual  
C:Keywords: tandem repeat

Query Match 33.3%; Score 11; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVP 3  
II  
Db 1 AAP 3

Search completed: September 13, 2003, 20:44:25  
Job time : 40 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model:

Run on: September 13, 2003, 20:41:40 ; Search time 22 Seconds  
(without alignments)  
14.963 Million cell updates/sec

Title: US-09-939-293a-19\_COPY\_56\_62  
Perfect score: 33  
Sequence: 1 AVPIAOK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues  
Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	15	45.5	6 1 EI01_LITRU	P82096 littoria rub
2	13	39.4	7 1 CARP_MYTED	P10420 mytilus edu
3	13	39.4	7 1 MNP1_LEPDE	P42884 lepidotars
4	12	36.4	6 1 OVM_LEPDE	P42885 lepidotars
5	11	33.3	5 1 SUGA_ACHDO	P19991 acheta dome
6	11	33.3	7 1 TPFY_PACDA	P83455 pachymedusa
7	10	30.3	5 1 BPP7_BOTIN	P30425 bothrops in
8	10	30.3	7 1 ALI3_CARMA	P81806 carcinus ma
9	10	30.3	7 1 ALI4_CARMA	P81807 carcinus ma
10	10	30.3	7 1 ALI5_CARMA	P81808 carcinus ma
11	10	30.3	7 1 TVS1_LITRU	P82065 littoria rub
12	9	27.3	6 1 VP19_HSVIK	P23210 herpes simp
13	8	24.2	5 1 EI03_LITRU	P82099 littoria rub
14	8	24.2	5 1 PRCT_PERAM	P01373 periplaneta
15	8	24.2	6 1 CIP1_MYTED	P13736 mytilus edu
16	8	24.2	6 1 CIP2_MYTED	P13737 mytilus edu
17	8	24.2	6 1 TRP1_PSEPU	P36414 pseudomonas
18	8	24.2	7 1 EI05_LITRU	P82101 littoria rub
19	8	24.2	7 1 UN06_PINPS	P81675 pinus pinas
20	7	21.2	3 1 THYL_PIG	P01151 sus scrofa
21	7	21.2	4 1 DCM1_PSECH	P19916 pseudomonas
22	7	21.2	4 1 RM01_YEAST	P36515 saccharomyc
23	7	21.2	4 1 TUFT_HUMAN	P01588 homo sapien
24	7	21.2	5 1 PAP2_PARMA	P81664 pardachirus
25	7	21.2	6 1 TMOF_SARBU	P41495 sarcophaga
26	7	21.2	7 1 CHOX_AICSP	P16101 alcaligenes
27	7	21.2	7 1 CIA_ENTFA	P11932 enterococcu
28	7	21.2	7 1 FAR1_HELTI	P41871 hellisoma tr
29	7	21.2	7 1 FAR4_PANRE	P41875 panagrellus
30	7	21.2	7 1 FAR6_CALYO	P41866 calliphora
31	7	21.2	7 1 GFPR_MOUSE	P99025 mus musculu
32	7	21.2	7 1 LANC_CARUI	P36660 carobacter
33	7	21.2	7 1 UF04_MOUSE	P38642 mus musculu

34	6	18.2	4 1 DCM5_PSECH	P19918 pseudomonas
35	6	18.2	6 1 UN06_CLOPA	P81351 clostridium
36	6	18.2	7 1 UF03_MOUSE	P38641 mus musculu
37	6	18.2	7 1 UH11_RAF	P56576 rattus norv
38	5	15.2	3 1 GRM4_HUMAN	P01157 homo sapien
39	5	15.2	3 1 LOXE_VIBFI	P24272 vibrio fisc
40	5	15.2	4 1 FFKA_ANTEL	P58705 anthopleura
41	5	15.2	5 1 B108_CITFR	P12997 citrobacter
42	5	15.2	5 1 EI04_LITRU	P82100 littoria rub
43	5	15.2	5 1 PSK_DAUCA	P58261 daucus caro
44	5	15.2	5 1 TRM3_ECOLI	P13973 escherichia
45	5	15.2	5 1 UF01_MOUSE	P38639 mus musculu

## ALIGNMENTS

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RESULT 1
EI01_LITRU          STANDARD;          PRT;          6 AA.
ID EI01_LITRU
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 1.
OS Littoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Littoria.
OX NCBI_Taxid=104695;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Webnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Littori electrica. Comparison with the skin peptides from Littoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 6 AA: 792 MW: 6683704772C9A000 CRC64;
SQ SEQUENCE 6 AA: 792 MW: 6683704772C9A000 CRC64;

Query Match          45.5%; Score 15; DB 1; Length 6;
Best local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPI 4
Db 2 VPI 4

RESULT 2
CARP_MYTED          STANDARD;          PRT;          7 AA.
ID CARP_MYTED
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_Taxid=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Muneoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia."
RL Brain Res. 422:374-376(1987).
CC -1- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)

```

CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS  
CC REFRACTORY MUSCLE.  
DR PIR: A29342; ECMOCR.  
KW Hormone: Amidation.  
FT MOD.RES  
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 7;  
Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVPI 4  
1:1:  
Db 1 AMPM 4

RESULT 3  
NMPI\_LEPDE  
ID NMPI\_LEPDE STANDARD; PRT; 7 AA.  
AC P42984;

DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DE 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Myotrophic neuropeptide 1 (Ied-MNP-1).  
OS Leptinotarsa decemlineata (Colorado potato beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Phyllophaga; Chrysomelidae; Chrysomelinae;  
OC Chrysomelini; Leptinotarsa.  
OX NCBI\_TaxId=7539;

RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE-Head;  
RX MEDLINE=95380343; PubMed=7651886;  
RA Spitaels K., Vankeerberghen A., Schoofs L., Torrekens S.,  
RA Grauwels L., Van Leuven F., de Loof A.;  
RT "Identification, characterization, and immunological localization of  
RT a novel myotrophic neuropeptide in the Colorado potato beetle,  
RT Leptinotarsa decemlineata.";  
RL Peptides 16:365-374(1995).  
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE  
CC OVIDUCT.  
KW Neuropeptide; Amidation.  
FT MOD.RES  
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 PLA 5  
1:1:  
Db 5 PLA 7

RESULT 4  
OVM\_LEPDE  
ID OVM\_LEPDE STANDARD; PRT; 6 AA.  
AC P42985;

DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DE 01-NOV-1995 (Rel. 32, Last annotation update)  
DE Oviductal motility stimulating peptide (Ied-OVM).  
OS Leptinotarsa decemlineata (Colorado potato beetle).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;  
OC Phyllophaga; Chrysomelidae; Chrysomelinae;  
OC Chrysomelini; Leptinotarsa.  
OX NCBI\_TaxId=7539;

RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE-Head;  
RX MEDLINE=91271080; PubMed=2052497;

RA Spitaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,  
RA Proost P., Torrekens S., de Loof A.;  
RT "Isolation, identification and synthesis of novel oviductal motility  
RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa  
RT decemlineata.";  
RL Peptides 12:31-36(1991).  
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE  
CC OVIDUCT.  
KW Neuropeptide; Amidation.  
FT MOD.RES  
SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;

Query Match 36.4%; Score 12; DB 1; Length 6;  
Best Local Similarity 75.0%; Pred. No. 1.3e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 IAOK 7  
1:1:  
Db 1 IAYK 4

RESULT 5  
SUGA\_ACHDO  
ID SUGA\_ACHDO STANDARD; PRT; 5 AA.  
AC P19991;

DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DE 01-OCT-1996 (Rel. 34, Last annotation update)  
DE Suboesophageal ganglion pentapeptide.  
OS Acheta domesticus (House cricket).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;  
OC Acheta.  
OX NCBI\_TaxId=6997;  
RN [1]  
RP SEQUENCE.  
RC Wicker C., Wicker C.;  
RT "Isolation and structure of a peptide isolated from the  
RT suboesophageal ganglion of Acheta domesticus (Orthoptera).";  
RL Comp. Biochem. Physiol. 88C:185-187(1987).  
CC -1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL  
CC GANGLIA.  
DR PIR: J50319; J50319.

Query Match 33.3%; Score 11; DB 1; Length 5;  
Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AVP 3  
1:1:  
Db 2 AVP 4

RESULT 6  
TPFY\_PACDA  
ID TPFY\_PACDA STANDARD; PRT; 7 AA.  
AC P83455;

DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DE 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Tryptophyllin-1 (Pdt-1).  
OS Pachymedusa dactiolor (Giant Mexican leaf frog).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
OC Phyllomedusinae; Pachymedusa.  
OX NCBI\_TaxId=75988;

RN [1]  
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF  
RP PRO-7.  
RC TISSUE-Skin secretion;  
RA Chen T.B., Orr D.F., Shaw C.;  
RX "Pachymedusa dactiolor tryptophyllin-1 (Pdt-1): structural

```

RT Characterization, pharmacological activity and cloning of precursor
RT CNA.
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -1- FUNCTION: Myosin. Has selective relaxing activity on vascular
CC smooth muscle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3 3
FT MOD_RES 7 7
FT MOD_RES 7 7
SQ SEQUENCE 7 AA: 794 MW: 7772D37DC7776350 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
DB 6 VP 7

RESULT 7
BPP7_BOTIN STANDARD; PRT; 5 AA.
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Quelama jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=90351557; Pubmed-2386615;
RA Cintria A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: G37196; G37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1
FT MOD_RES 1 1
SQ SEQUENCE 5 AA: 629 MW: 776DC37326B00000 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OK 7
DB 1 OK 2

RESULT 8
ALL3_CARMA STANDARD; PRT; 7 AA.
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Carcinus maenas (Common shore crab) (Green crab).

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OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and thoracic ganglion;
RX MEDLINE=98121193; Pubmed-9461295;
RA Dve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thore A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 7 AA: 796 MW: 672879CDBC8476B70 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PIA 5
DB 2 PIA 4

RESULT 9
ALL4_CARMA STANDARD; PRT; 7 AA.
AC P81807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and thoracic ganglion;
RX MEDLINE=98121193; Pubmed-9461295;
RA Dve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thore A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 7 AA: 782 MW: 672879CDBC8476AC0 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PIA 5
DB 2 PIA 4

RESULT 10
ALL5_CARMA STANDARD; PRT; 7 AA.
AC P81808;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinus maenas (Common shore crab) (Green crab).
OS Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

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OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;  
 OC Eubrachyura; Fortunoidae; Fortunidae; Carcinus.  
 OX NCBI\_TaxID=6759;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Cerebral ganglion, and Thoracic ganglion;  
 RX MEDLINE=98121193; PubMed=9461295;  
 RA Duvé H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaroš P.P.,  
 RA Thorpe A.;  
 RA "Isolation and identification of multiple neuropeptides of the  
 RT allatostatin superfamily in the shore crab *Carcinus maenas*.";  
 RL Eur. J. Biochem. 250:727-734(1997).  
 CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.  
 CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.  
 CC Neuropeptide; Amidation; Multigene family.  
 KM MOD\_RES 7  
 FT AMIDATION.  
 SQ SEQUENCE 7 AA; 781 MW; 672879CDB476420 CRC64;  
 Query Match 30.3%; Score 10; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.3e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 3 PIA 5  
 DB 2 PYA 4  
 RESULT 11  
 TY51\_LITRU STANDARD; PRT; 7 AA.  
 ID TY51\_LITRU  
 AC P82065;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Trypophyllin 5.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE-Skin secretion;  
 RA Steinboerner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RA "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAH.  
 KM Amphibian defense peptide; Amidation; Neuropeptide;  
 KM Pyroglutamate carboxylic acid.  
 FT MOD\_RES 1  
 FT PYROGLUTAMATE CARBOXYLIC ACID.  
 FT AMIDATION.  
 SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;  
 Query Match 30.3%; Score 10; DB 1; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 VP 3  
 DB 2 IP 3  
 RESULT 12  
 VP19\_HSV1K STANDARD; PRT; 6 AA.  
 ID VP19\_HSV1K  
 AC P23210;  
 DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)  
 DT 01-DEC-1992 (Rel. 24, Last annotation update)  
 DE Capsid assembly and DNA maturation protein (Virion protein UL38)  
 DE (Capsid protein VP19C) (Fragment).  
 GN UL38.  
 OS Herpes simplex virus (type 1 / strain KOS).  
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;  
 OC Alphaherpesvirinae; Simplexvirus.  
 OX NCBI\_TaxID=10306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91101287; PubMed=1846198;  
 RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,  
 RA Silverstein S., Wagner E.K.;  
 RA "Analysis of the herpes simplex virus type 1 promoter controlling the  
 RT expression of UL38, a true late gene involved in capsid assembly.";  
 RL J. Virol. 65:769-786(1991).  
 CC -1- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSID ARE  
 CC EMBEDDED. BINDS DNA.  
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL: M57646; AAA45830.1; -  
 KM Capsid assembly; Coat protein; DNA-binding.  
 FT NON\_TER 6  
 SQ SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;  
 Query Match 27.3%; Score 9; DB 1; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 PI 4  
 DB 5 PL 6  
 RESULT 13  
 E103\_LITRU STANDARD; PRT; 5 AA.  
 ID E103\_LITRU  
 AC P82099;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 15-SEP-2003 (Rel. 42, Last annotation update)  
 DE Electrin 3.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 OC Pelodyadinae; Litoria.  
 OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE-Skin secretion;  
 RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
 RA "Peptides from the skin glands of the Australian buzzing tree frog  
 RT 'Litoria rubella'. Comparison with the skin peptides from Litoria  
 RT rubella.";  
 RL Aust. J. Chem. 52:639-645(1999).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Skin.  
 KM Amphibian defense peptide; Amidation.  
 FT MOD\_RES 5  
 FT AMIDATION.  
 SQ SEQUENCE 5 AA; 630 MW; 668761P2C9A00000 CRC64;  
 Query Match 24.2%; Score 8; DB 1; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 PI 4  
1:  
DB 4 PM 5

## RESULT 14

PROCT\_PERAM STANDARD; PRT; 5 AA.  
ID PROCT\_PERAM STANDARD; PRT; 5 AA.  
AC P01373;  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 01-FEB-1995 (Rel. 31, Last annotation update)  
DE Proctolin.  
OS Periplaneta americana (American cockroach),  
OS Limulus polyphemus (Atlantic horseshoe crab), and  
OS Carcinus maenas (Common shore crab) (Green crab).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattellidae;  
OC Blattidae; Periplaneta.  
OX NCBI\_TaxID=6978, 6850, 6759;  
RN [1]  
RP SEQUENCE.  
RC SPECIES-P.americana;  
RX MEDLINE=76074708; PubMed=576;  
RA Starratt A.N., Brown B.E.;  
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter  
in insects.";  
RL Life Sci. 17:1253-1256(1975).  
RN [2]  
RP BIOLOGICAL SOURCE.  
RC SPECIES-P.americana;  
RX MEDLINE=81225865; PubMed=6113690;  
RA O'Shea M., Adams M.E.;  
RT "Pentapeptide (proctolin) associated with an identified neuron.";  
RL Science 213:567-569(1981).  
RN [3]  
RP SEQUENCE.  
RC SPECIES-L.polyphemus;  
RX MEDLINE=90287800; PubMed=2356151;  
RA Groome J.R., Tillinphast E.R., Townley M.A., Vetrovs A.,  
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,  
RA Shabanowitz J.;  
RT "Identification of proctolin in the central nervous system of the  
horseshoe crab, Limulus polyphemus.";  
RL Peptides 11:205-211(1990).  
RN [4]  
RP SEQUENCE.  
RC SPECIES-C.maenas;  
RX MEDLINE=8632789; PubMed=2872661;  
RA Stangier J., Dirksen H., Keller R.;  
RT "Identification and immunocytochemical localization of proctolin in  
pericardial organs of the shore crab, Carcinus maenas.";  
RL Peptides 7:67-72(1986).  
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,  
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.  
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN  
THE CRAB PERICARDIAL ORGANS.  
CC PIR: A01644; HOROA.  
DR PIR: A60411; A60411.  
KW Neuropeptide.  
SQ SEQUENCE 5 AA: 649 MW: 718767384600000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VP 3  
1:  
DB 3 LP 4

RESULT 15

CIP1\_MYTED  
ID CIP1\_MYTED STANDARD; PRT; 6 AA.  
AC P13736;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-JAN-1990 (Rel. 13, Last sequence update)  
DT 15-DEC-1998 (Rel. 37, Last annotation update)  
DE Contraction-inhibiting peptide I (MIP I).  
OS Mytilus edulis (Blue mussel).  
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytilloidea;  
OC Mytilloidea; Mytilidae; Mytilus.  
OX NCBI\_TaxID=6550;  
RN [1]  
RP SEQUENCE.  
RC TISSUE-Pedal ganglion;  
RX MEDLINE=88240357; PubMed=337776;  
RA Hirata T., Kubota I., Iwasawa N., Takahatake I., Ikeda T., Muneoka Y.;  
RT "Structures and actions of Mytilus inhibitory peptides.";  
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).  
CC -1- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN  
MUSCLES.  
CC -1- SIMILARITY: TO MIP II.  
DR PIR: A27696; A27696.  
KW Hormone; Amidation.  
FT MOD\_RES 6  
SQ SEQUENCE 6 AA: 637 MW: 72096877581000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 6;  
Best Local Similarity 50.0%; Pred. No. 1.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 PI 4  
1:  
DB 3 PM 4

Search completed: September 13, 2003, 20:42:13  
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: September 13, 2003, 20:41:40 ; Search time 93 Seconds  
(without alignments)  
19.423 Million cell updates/sec

Title: US-09-939-293a-19\_COPY\_56\_62  
Perfect score: 33  
Sequence: 1 AVPIAOK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 67

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: SP\_ARCHAEA:\*
- 2: SP\_BACTERIA:\*
- 3: SP\_FUNGI:\*
- 4: SP\_HUMAN:\*
- 5: SP\_INVERTEBRATE:\*
- 6: SP\_MAMMAL:\*
- 7: SP\_MNC:\*
- 8: SP\_ORGANELLE:\*
- 9: SP\_PHAGE:\*
- 10: SP\_PLANT:\*
- 11: SP\_RODENT:\*
- 12: SP\_VIRUS:\*
- 13: SP\_VERTEBRATE:\*
- 14: SP\_UNCLASSIFIED:\*
- 15: SP\_VIRUS:\*
- 16: SP\_BACTERIAP:\*
- 17: SP\_ARCHAEP:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	13	39.4	7 13	042564
2	11	33.3	7 2	050556
3	11	33.3	7 4	08NH7
4	11	33.3	7 15	007624
5	10	30.3	5 10	099007
6	10	30.3	5 13	P83308
7	10	30.3	7 6	Q28742
8	10	30.3	7 10	P93233
9	8	24.2	7 2	047477
10	8	24.2	7 2	P72081
11	8	24.2	7 2	054248
12	8	24.2	7 7	095945
13	8	24.2	7 11	063668
14	8	24.2	7 12	066113
15	7	21.2	6 10	P82181
16	7	21.2	6 10	P82182

17	7	21.2	7 8	P92214	P92214 amblyopyrum
18	7	21.2	7 8	P92393	P92393 hordeum vul
19	7	21.2	7 8	P92403	P92403 lophopyrum
20	7	21.2	7 8	P92427	P92427 peridictyon
21	7	21.2	7 8	P92430	P92430 begliopsis ta
22	7	21.2	7 8	P92221	P92221 bromus lner
23	7	21.2	7 8	098866	098866 spinacia ol
24	7	21.2	7 8	P92425	P92425 pseudoroegn
25	7	21.2	7 8	P92381	P92381 hordeum bra
26	7	21.2	7 8	P92387	P92387 henardia p
27	7	21.2	7 8	P92210	P92210 agropyron c
28	7	21.2	7 8	P92440	P92440 thnopyrum
29	7	21.2	7 8	P92218	P92218 australopyr
30	7	21.2	7 8	P92390	P92390 heteranthel
31	7	21.2	7 8	P92372	P92372 haynaldia v
32	7	21.2	7 8	P92442	P92442 taenlatheru
33	7	21.2	7 8	P92226	P92226 crithopsis
34	7	21.2	7 8	08MRY6	08MRY6 taraxacum (
35	7	21.2	7 8	P92385	P92385 hordeum mar
36	7	21.2	7 8	P92421	P92421 psathyrosta
37	7	21.2	7 12	066205	066205 transmissib
38	7	21.2	7 15	08JEB81	08JEB81 human immun
39	6	18.2	6 10	P82541	P82541 spinacia ol
40	6	18.2	7 2	047029	047029 enterobacte
41	6	18.2	7 2	08GL00	08GL00 borrelia bu
42	6	18.2	7 4	015903	015903 homo sapien
43	6	18.2	7 4	015897	015897 homo sapien
44	6	18.2	7 10	P82445	P82445 nicotiana t
45	6	18.2	7 11	08K3H6	08K3H6 rattus norv

# ALIGNMENTS

RESULT 1					
ID	042564	PRELIMINARY:	PRT:	7	AA.
AC	042564:				
DT	01-JAN-1998 (TREMREL. 05, Created)				
DT	01-JAN-1998 (TREMREL. 05, Last sequence update)				
DT	01-NOV-1998 (TREMREL. 08, Last annotation update)				
DE	Truncated voltage-gated sodium channel alpha subunit (Fragment).				
GN	SCN8A.				
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;				
OC	Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;				
OC	Tetraodontidae; Tetraodontidae; Takifugu.				
OX	NCBI_TaxID=31033;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=97442476; PubMed=9295353;				
RA	Plummer N.W., McBurney M.W., Meisler M.H.;				
RT	*Alternative splicing of the sodium channel SCN8A predicts a truncated				
RT	two-domain protein in fetal brain and non-neuronal cells.*;				
RL	J. Biol. Chem. 272:24008-24015(1997).				
DR	EMBL; U97673; AAB80916.1; -				
KW	IONIC channel.				
FT	NON_TER				
SO	SEQUENCE	7	AA:	730	MM; 75B72EA2C73772A0 CRC64;
QY	Query Match	39.4%;	Score	13;	DB 13; Length 7;
DB	Best Local Similarity	66.7%;	Pred.	No. 8.3e+05;	
	Matches	2;	Conservative	1;	Mismatches 0; Indels 0; Gaps 0;
RESULT 2					
ID	050556	PRELIMINARY:	PRT:	7	AA.

AC 050556;  
DT 01-JUN-1998 (TREMBLrel. 06, Created)  
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE g1ya (Fragment).  
GN GLYA.  
OS Actinobacillus actinomycetemcomitans (Haemophilus  
OC actinomycetemcomitans).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
OC Pasteurellaceae; Actinobacillus.  
OX NCBI\_TaxID=714;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ATCC 33384;  
RX MEDLINE=96355846; PubMed=8751884;  
RA Koldiridze D., Spliznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,  
RT Kralig E.;  
RT "cls Elements and trans factors are both important in strain-specific  
RT regulation of the leukotoxin gene in Actinobacillus  
RT actinomycetemcomitans".  
RL Infect Immun. 64:3451-3460(1996).  
DR EMBL; 051862; AAB8721.1; -.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 33.3%; Score 11; DB 2; Length 7;  
Best Local Similarity 33.3%; Pred. No. 8.3e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPI 4  
DB 3 LPV 5

RESULT 3  
Q8NH7 PRELIMINARY; PRT; 7 AA.  
AC Q8NH7;  
DT 01-OCT-2002 (TREMBLrel. 22, Created)  
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)  
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)  
DE Minl-cistron.  
GN NHE3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Malakooti J., Ramaswamy K.;  
RT "Molecular cloning and characterization of the human Na+/H+ exchanger  
RT NHE-3 gene promoter region".  
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF282824; AAM53436.1; -.  
SQ SEQUENCE 7 AA; 842 MW; 74072DC772DA06F0 CRC64;

Query Match 33.3%; Score 11; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VP 3  
DB 3 VP 4

RESULT 4  
Q07624 PRELIMINARY; PRT; 7 AA.  
AC Q07624;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE UORF1.

OS Rous sarcoma virus (strain Prague C).  
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.  
OX NCBI\_TaxID=11888;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93010967; PubMed=1327749;  
RA Donze O., Spahr P.F.;  
RT "Role of the open reading frames of Rous sarcoma virus leader RNA in  
RT translation and genome packaging".  
RL EMBO J. 11:3747-3757(1992).  
DR EMBL; X67587; CAA47862.1; -.  
SQ SEQUENCE 7 AA; 672 MW; 776045A7687DD6F0 CRC64;

Query Match 33.3%; Score 11; DB 15; Length 7;  
Best Local Similarity 33.3%; Pred. No. 8.3e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVP 3  
DB 5 STP 7

RESULT 5  
Q99007 PRELIMINARY; PRT; 5 AA.  
AC Q99007;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE Alpha amylase (Fragment).  
GN AMY GENE.  
OS Hordeum vulgare (Barley).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
OC Triliceae; Hordeum.  
OX NCBI\_TaxID=4513;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91329704; PubMed=1831055;  
RA Jacobsen J.V., Close T.J.;  
RT "Control of transient expression of chimaeric genes by gibberellic  
RT acid and abscisic acid in protoplasts prepared from mature barley  
RT aleurone layers".  
RL Plant Mol Biol. 16:713-721(1991).  
DR EMBL; X54643; CAA38455.1; -.  
FT NON\_TER  
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 30.3%; Score 10; DB 10; Length 5;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 INAK 7  
DB 1 MANK 4

RESULT 6  
P83308 PRELIMINARY; PRT; 5 AA.  
AC P83308;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE FMRFamide-like neuropeptide (LPLRF-amide).  
OS Gallus gallus (chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE, AND SYNTHESIS.  
RC TISSUE=Brain;

```
RX PubMed-6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRFamide.";
RL Nature 305:328-330(1983).
CC -1- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
CC Neuropeptide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match
Best Local Similarity 30.3%; Score 10; DB 13; Length 5;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPI 4
   1:
Db 1 LPL 3

RESULT 7
ID 028742 PRELIMINARY; PRT; 7 AA.
AC 028742;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-84221901; PubMed-6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1A1E69326B0 CRC64;

Query Match
Best Local Similarity 30.3%; Score 10; DB 6; Length 7;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OK 7
   1 1
Db 1 OK 2

RESULT 8
ID P93233 PRELIMINARY; PRT; 7 AA.
AC P93233;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
DE (Fragment).
GN LE-ACS1B.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97351561; PubMed-9207843;
RA Oetliker J.H., Olson D.C., Shu O.Y., Yang S.F.;
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
```

```
RT synthase genes by elicitor in suspension cultures of tomato
RT (Lycopersicon esculentum).";
RL Plant Mol. Biol. 34:275-286(1997).
DR EMBL; U75692; AAC49682.1; -.
KW lyase.
FT NON_TER 1
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match
Best Local Similarity 25.0%; Score 10; DB 10; Length 7;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PIAQ 6
   1:
Db 3 PLVR 6

RESULT 9
ID 047477 PRELIMINARY; PRT; 7 AA.
AC 047477;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-MAY-1999 (TREMblrel. 10, last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, last annotation update)
DE Tpi protein (Fragment).
GN TPI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE OF 7-7 FROM N.A.
RX MEDLINE-85203917; PubMed-3158524;
RA Hellinga H.W., Evans P.R.;
RT "Nucleotide sequence and high-level expression of the major
RT Escherichia coli phosphofructokinase.";
RL Eur. J. Biochem. 149:363-373(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Evans P.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X02519; CAA26359.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDB1DB0 CRC64;

Query Match
Best Local Similarity 24.2%; Score 8; DB 2; Length 7;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AQR 7
   1 1
Db 3 AAK 5

RESULT 10
ID P72081 PRELIMINARY; PRT; 7 AA.
AC P72081;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE 3'-methylcephem hydroxylase (Fragment).
GN CEF3.
OS Nocardia lactamdurans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiales; Amycolatopsia.
OX NCBI_TaxID=1913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96009872; PubMed-7557411;
RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
RA Liras P.;
RT "Characterization of the cmh genes of Nocardia lactamdurans and
```

RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem  
RT O-carbamoyltransferase for cephamycin biosynthesis."  
RL Gene 162:21-27(1995).  
DR EMBL; 221682; CAA79797.1; -.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;  
Query Match 24.2%; Score 8; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AV 2  
11  
DB 4 AV 5  
RESULT 11  
ID 054248 PRELIMINARY; PRT; 7 AA.  
AC 054248;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE RplO protein (Fragment).  
GN RplO.  
OS Streptomyces griseus.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_Taxid=1911;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N2-3-11;  
RX MEDLINE=20011291; PubMed=10542330;  
RA Poehling S., Piepersberg W., Wehmeier U.F.;  
RT "Analysis and regulation of the sec Y gene from Streptomyces griseus  
RT N2-3-11 and interaction of the sec Y protein with the SecA protein."  
RL Biochim. Biophys. Acta 1447:298-302(1999).  
DR EMBL; X95915; CAA65160.1; -.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;  
Query Match 24.2%; Score 8; DB 2; Length 7;  
Best Local Similarity 20.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 2 VP1A 6  
11  
DB 1 VTYTE 5  
RESULT 12  
ID 095945 PRELIMINARY; PRT; 7 AA.  
AC 095945;  
DT 01-FEB-1997 (TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Inside intron 5 (Fragment).  
OS Saccharomyces cerevisiae (Baker's yeast).  
OG Mitochondrion.  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_Taxid=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=D273-10B;  
RX MEDLINE=81069885; PubMed=6254986;  
RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;  
RT "Assembly of the mitochondrial membrane system: Structure and  
RT nucleotide sequence of the gene coding for subunit I of yeast  
RT cytochrome oxidase."  
RL J. Biol. Chem. 255:11927-11941(1980).  
DR EMBL; V00694; CAA24066.1; -.  
FT

KW Mitochondrion.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 859 MW; 75B723362DCDC460 CRC64;  
Query Match 24.2%; Score 8; DB 8; Length 7;  
Best Local Similarity 100.0%; Pred. No. 8.3e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AV 2  
11  
DB 2 AV 3  
RESULT 13  
ID 063668 PRELIMINARY; PRT; 7 AA.  
AC 063668;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ORF2 protein.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Kidney;  
RX MEDLINE=95396550; PubMed=7667072;  
RA Mandon B., Bellanger A.C., Elalouf J.M.;  
RT "Inverse-PCR-mediated cloning of the promoter for the rat vasopressin  
RT V2 receptor gene."  
RL Pflugers Arch. 430:12-18(1995).  
DR EMBL; X83264; CAA58237.1; -.  
FT NON\_TER  
SQ SEQUENCE 7 AA; 703 MW; 75A767287DC6D6F0 CRC64;  
Query Match 24.2%; Score 8; DB 11; Length 7;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 2 VP 3  
11  
DB 5 LP 6  
RESULT 14  
ID 066113 PRELIMINARY; PRT; 7 AA.  
AC 066113;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE C-terminus of the viral replicase (Fragment).  
OS Cherry leaf roll virus.  
OS Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;  
OC Nepovirus.  
OX NCBI\_Taxid=12615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=walnut;  
RL Borja M.;  
RT Thesis (1992). Biologia Molecular y Virologia Vegetal, CIT-INIA.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=walnut;  
RX MEDLINE=96124520; PubMed=8560786;  
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;  
RT "Long, nearly identical untranslated sequences at the 3' terminal  
RT regions of the genomic RNAs of cherry leafroll virus (walnut  
RT strain)."  
RL Virus Genes 10:245-252(1995).  
DR EMBL; Z34265; CAA84019.1; -.  
FT NON\_TER  
SQ SEQUENCE 1

SO SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 24.2%; Score 8; DB 12; Length 7;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VP 3  
1  
5 LP 6

## RESULT 15

P82181 PRELIMINARY; PRT; 6 AA.  
AC P82181;  
DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)  
DE Chloroplast 50S ribosomal protein L10 beta (fragment).  
OS Spinacia oleracea (Spinach).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OC Caryophyllales; Caryophyllaceae; Spinacia.  
OX NCBI\_TaxID=3562;  
RN [1]  
RP SEQUENCE.  
RC STRAIN=cv. ALVARO; TISSUE=leaf;  
RX MEDLINE=20435798; PubMed=10874046;  
RA Yamaguchi K., Subramanian A.R.;  
RT "The plastid ribosomal proteins. Identification of all the proteins in  
the 50 S subunit of an organelle ribosome (chloroplast).";  
RL J. Biol. Chem. 275:28466-28482(2000).  
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.  
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.  
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.  
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
DR InterPro: IPR001790; Ribosomal\_L10.  
DR Pfam: PF00466; Ribosomal\_L10; PARTIAL.  
DR PROSITE: PS01109; RIBOSOMAL\_L10; PARTIAL.  
KW Ribosomal protein; Chloroplast; rRNA-binding.  
FT NON\_TER  
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 21.2%; Score 7; DB 10; Length 6;  
Best Local Similarity 50.0%; Pred. No. 8.3e+05;  
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AV 2  
1  
1 AI 2

Search completed: September 13, 2003, 20:46:08  
Job time : 97 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 13, 2003, 20:41:41 ; Search time 29 Seconds  
(without alignments)  
10.213 Million cell updates/sec

Title: US-09-939-293a-19\_COPY\_56\_62  
Perfect score: 33  
Sequence: 1 AVPIAOK 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 49738

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/1aa/Backfile.sl7.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	66.7	7	2	US-08-819-013-3
2	20	60.6	7	4	US-08-313-127A-10
3	20	60.6	7	4	US-09-492-766-8
4	18	54.5	4	2	US-08-592-646A-60
5	18	54.5	4	4	US-09-165-422-60
6	18	54.5	5	6	5217869-41
7	18	54.5	5	6	5217869-90
8	18	54.5	6	1	US-08-325-509-46
9	18	54.5	6	1	US-08-584-579-1
10	18	54.5	7	3	US-09-121-964-7
11	17	51.5	4	6	5496927-1
12	17	51.5	6	6	5496927-2
13	17	51.5	7	1	US-08-618-693-96
14	17	51.5	7	3	US-08-973-124-185
15	17	51.5	7	3	US-08-991-743C-96
16	17	51.5	7	4	US-08-983-075D-13
17	17	51.5	7	4	US-09-638-202A-32
18	17	51.5	7	4	US-08-843-076D-37
19	17	51.5	7	4	US-09-851-486-96
20	17	51.5	7	5	PCT-US96-0801A-185
21	16	48.5	4	3	US-09-357-952-46
22	16	48.5	4	4	US-09-521-650-46
23	16	48.5	4	4	US-09-168-888-46
24	16	48.5	4	4	US-09-513-783A-84
25	16	48.5	5	2	US-08-667-001-24
26	16	48.5	5	3	US-08-485-324-21
27	16	48.5	5	3	US-08-447-506-21

28	16	48.5	5	3	US-08-235-437-21	Sequence 21, App1
29	16	48.5	5	3	US-08-447-515-21	Sequence 21, App1
30	16	48.5	5	6	5217869-92	Patent No. 5217869
31	16	48.5	6	3	US-08-802-981-187	Sequence 187, App
32	16	48.5	6	4	US-09-007-288E-17	Sequence 17, App1
33	16	48.5	6	4	US-09-007-288E-158	Sequence 158, App
34	16	48.5	6	4	US-09-007-288E-159	Sequence 159, App
35	16	48.5	6	4	US-09-007-288E-160	Sequence 160, App
36	16	48.5	7	1	US-08-078-090-5	Sequence 5, App1
37	16	48.5	7	3	US-08-891-271-5	Sequence 5, App1
38	16	48.5	7	3	US-09-103-478-5	Sequence 5, App1
39	16	48.5	7	3	US-09-103-478-17	Sequence 17, App1
40	16	48.5	7	4	US-09-193-931C-5	Sequence 5, App1
41	16	48.5	7	4	US-09-193-931C-17	Sequence 17, App1
42	16	48.5	7	4	US-09-400-653A-3	Sequence 3, App1
43	16	48.5	7	4	US-09-400-653A-4	Sequence 4, App1
44	16	48.5	7	4	US-09-248-061B-3	Sequence 3, App1
45	16	48.5	7	4	US-09-248-061B-4	Sequence 4, App1

## ALIGNMENTS

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RESULT 1
US-08-819-013-3
; Sequence 3, Application US/08819013
; Patent No. 5994522
;
GENERAL INFORMATION:
;
APPLICANT: Chan, Andrew C.
;
TITLE OF INVENTION: BLNK PROTEINS
;
NUMBER OF SEQUENCES: 13
;
CORRESPONDENCE ADDRESS:
;
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
;
STREET: Four Embarcadero Center, Suite 3400
;
CITY: San Francisco
;
STATE: California
;
COUNTRY: United States
;
ZIP: 94111-4187
;
COMPUTER READABLE FORM:
;
MEDIUM TYPE: Floppy disk
;
OPERATING SYSTEM: IBM PC compatible
;
SOFTWARE: PatentIn Release #1.0, Version #1.30
;
CURRENT APPLICATION DATA:
;
APPLICATION NUMBER: US/08/819,013
;
FILING DATE: 17-MAR-1997
;
CLASSIFICATION: 435
;
PRIOR APPLICATION DATA:
;
APPLICATION NUMBER: US 08/788,322
;
FILING DATE: 24-JAN-1997
;
ATTORNEY/AGENT INFORMATION:
;
NAME: Silva, Robin M.
;
REGISTRATION NUMBER: 38,304
;
REFERENCE/DOCKET NUMBER: A-64383-1/RFT/RMS
;
TELECOMMUNICATION INFORMATION:
;
TELEPHONE: (415) 781-1989
;
TELEFAX: (415) 398-3249
;
TELEX: 910 277299
;
INFORMATION FOR SEQ. ID NO.: 3:
;
SEQUENCE CHARACTERISTICS:
;
LENGTH: 7 amino acids
;
TYPE: amino acid
;
STRANDEDNESS: unknown
;
TOPOLOGY: unknown
;
MOLECULE TYPE: protein
;
US-08-819-013-3
;
Query Match 66.7%; Score 22; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 2 VP1AOK 7
:|:|

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Db 2 IPVLOK 7

RESULT 2  
US-08-313-127A-10  
; Sequence 10, Application US/08313127A  
; Patent No. 5618699  
; GENERAL INFORMATION:  
; APPLICANT: HAMAMOTO, Hiroshi  
; APPLICANT: SUGIYAMA, Yoshinori  
; APPLICANT: NAKAGAWA, No. 56186991aki  
; APPLICANT: HASHIDA, Elji  
; APPLICANT: TSUCHIMOTO, Suguru  
; APPLICANT: NAKANISHI, No. 56186991yuki  
; APPLICANT: MATSUNAGA, Yuji  
; APPLICANT: OKADA, Yoshimi  
; TITLE OF INVENTION: PLANT VIRUS VECTOR, PLASMID,  
; TITLE OF INVENTION: PROCESS FOR EXPRESSION OF  
; TITLE OF INVENTION: FOREIGN GENE AND PROCESS FOR  
; TITLE OF INVENTION: OBTAINING FOREIGN GENE PRODUCT  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEARS  
; STREET: 2100 PENNSYLVANIA AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20037  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/313.127A  
; FILING DATE: 30-SEPT-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/JP 93/00408  
; FILING DATE: 31-MAR-1994  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 293-7060  
; TELEFAX: (202) 293-7860  
; TELEX: 6491103  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-313-127A-10

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Best Local Similarity 57.1%; Pred. No. 2.5e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVPIAQ 7  
1111:  
Db 1 AVYPQR 7

RESULT 3  
US-09-492-766-8  
; Sequence 8, Application US/09492766  
; Patent No. 6506732  
; GENERAL INFORMATION:  
; APPLICANT: AMICH, Jean  
; TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS  
; FILE REFERENCE: 6013-57"US"  
; CURRENT APPLICATION NUMBER: US/09/492.766  
; CURRENT FILING DATE: 2000-01-27  
; EARLIER APPLICATION NUMBER: 60/117,661

EARLIER FILING DATE: 1999-01-28  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 8  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk  
; OTHER INFORMATION: proteins  
US-09-492-766-8

Query Match 60.6%; Score 20; DB 4; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VPIAQ 7  
1111:  
Db 2 LPVPQR 7

RESULT 4  
US-08-592-646A-60  
; Sequence 60, Application US/08592646A  
; Patent No. 5851335  
; GENERAL INFORMATION:  
; APPLICANT: JOLIVET-REYNAUD, Colette  
; TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOXOPLASMA  
; TITLE OF INVENTION: GONDII AND APPLICATIONS  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: OLIVE & BERRIDGE, PLC  
; STREET: P.O. Box 19928  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/592.646A  
; FILING DATE: 26-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berridge, William P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPB 36923  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703 836-6400  
; TELEFAX: 703 836-2787  
; INFORMATION FOR SEQ ID NO: 60:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-592-646A-60

Query Match 54.5%; Score 18; DB 2; Length 4;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PIAQ 6  
1111:  
Db 1 PIAQ 4

RESULT 5  
US-09-165-422-60



; Sequence 60, Application US/09165422  
; Patent No. 6372897  
; GENERAL INFORMATION:  
; APPLICANT: JOLIVET-REYNAUD, Colette  
; TITLE OF INVENTION: MINOTOPIC POLYPEPTIDES OF TOXOPLASMA  
; REAGENTS  
; NUMBER OF SEQUENCES: 63  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: OLIFF & BERRIDGE, PLC  
; STREET: P.O. Box 19928  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22320  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/165,422  
; FILING DATE: 02-Oct-1998  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Berridge, William P.  
; REGISTRATION NUMBER: 30,024  
; REFERENCE/DOCKET NUMBER: WPB 36923  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703 836-6400  
; TELEFAX: 703 836-2787  
; INFORMATION FOR SEQ ID NO: 60:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; SEQUENCE DESCRIPTION: SEQ ID NO: 60:  
US-09-165-422-60  
  
Query Match 54.5%; Score 18; DB 4; Length 4;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 PIAQ 6  
1:11  
1 PLAQ 4  
Db  
  
RESULT 6  
5217869-41  
; Patent No. 5217869  
; APPLICANT: KAVVAR, LAWRENCE M.  
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC  
; REAGENTS  
; NUMBER OF SEQUENCES: 121  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/255,906  
; FILING DATE: 11-OCT-1988  
; SEQ ID NO: 41:  
; LENGTH: 5  
5217869-41  
  
Query Match 54.5%; Score 18; DB 6; Length 5;  
Best Local Similarity 60.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 AVPIA 5  
1:11  
1 AAPVA 5  
Db  
  
RESULT 7

5217869-90  
; Patent No. 5217869  
; APPLICANT: KAVVAR, LAWRENCE M.  
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC  
; REAGENTS  
; NUMBER OF SEQUENCES: 121  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/255,906  
; FILING DATE: 11-OCT-1988  
; SEQ ID NO: 90:  
; LENGTH: 5  
5217869-90  
  
Query Match 54.5%; Score 18; DB 6; Length 5;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 3 PIAQ 6  
1:11  
1 PLAQ 4  
Db  
  
RESULT 8  
US-08-325-509-46  
; Sequence 46, Application US/08325509  
; Patent No. 5543308  
; GENERAL INFORMATION:  
; APPLICANT: MORGAN, RICHARD D.  
; TITLE OF INVENTION: ISOLATED DNA ENCODING THE PseI  
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND RELATED METHODS FOR  
; NUMBER OF SEQUENCES: 55  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND  
; ADDRESS: BIOLABS, INC.  
; STREET: 32 TOZER ROAD  
; CITY: BEVERLY  
; STATE: MASSACHUSETTS  
; COUNTRY: US  
; ZIP: 01915  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/325,509  
; FILING DATE: 18-OCT-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILLIAMS, GREGORY D.  
; REGISTRATION NUMBER: 30901  
; REFERENCE/DOCKET NUMBER: NEB-104  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (508) 927-5054  
; TELEFAX: (508) 927-1705  
; INFORMATION FOR SEQ ID NO: 46:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: protein  
US-08-325-509-46  
  
Query Match 54.5%; Score 18; DB 1; Length 6;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AVPI 4  
1:11  
3 AVPI 6  
Db

RESULT 9  
US-08-584-579-1  
; Sequence 1, Application US/08584579  
; Patent No. 5674979  
; GENERAL INFORMATION:  
; APPLICANT: Schramm, Wolfgang  
; TITLE OF INVENTION: Agent for Inhibiting Symmetrical  
; TITLE OF INVENTION: Proteins, in Particular Enzymes  
; NUMBER OF SEQUENCES: 20  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
; STREET: 1201 New York Avenue N.W., Suite 1000  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/584,579  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/332,447  
; FILING DATE: 31-OCT-1994  
; APPLICATION NUMBER: US 08/112,215  
; FILING DATE: 26-AUG-1993  
; APPLICATION NUMBER: US 07/976,003  
; FILING DATE: 13-NOV-1992  
; APPLICATION NUMBER: US 07/585,141  
; FILING DATE: 07-DEC-1990  
; APPLICATION NUMBER: WO PCT/EP90/00219  
; FILING DATE: 09-FEB-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: DE P 39 04 040.2  
; FILING DATE: 10-FEB-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Imnen, Jeffrey L.  
; REGISTRATION NUMBER: 28957  
; REFERENCE/DOCKET NUMBER: 18644-96040  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: YES  
; US-08-584-579-1  
Query Match 54.5%; Score 18; DB 1; Length 6;  
Best Local Similarity 80.0%; Pred. No. 2.5e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 AVPIA 5  
; 1 1 1 1  
; 1 1 1 1  
DB 2 APPIA 6  
RESULT 10  
US-09-121-964-7  
; Sequence 7, Application US/09121964  
; Patent No. 6124447  
; GENERAL INFORMATION:  
; APPLICANT: Natoli, Shunji  
; TITLE OF INVENTION: NOVEL ENZYME CATALYZING DEPHOSPHORYLATION

; FILE REFERENCE: 32290-144753  
; CURRENT APPLICATION NUMBER: US/09/121,964  
; CURRENT FILING DATE: 1998-07-24  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Sarcophaga peregrina  
US-09-121-964-7  
Query Match 54.5%; Score 18; DB 3; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVPI 4  
; 1 1 1 1  
; 1 1 1 1  
DB 1 AVPIV 4  
RESULT 11  
5496927-1  
; Patent No. 5496927  
; APPLICANT: KOLB, H.MICHAEL, BURKHART, JOSEPH P.; JUNG, MICHEL J.;  
; GERHART, FRITZ E.; GIROUX, EUGENE L.; NEISES, BERNHARD; SCHIRLIN,  
; DANIEL G.  
; TITLE OF INVENTION: PEPTIDASE INHIBITORS  
; NUMBER OF SEQUENCES: 26  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/248,847  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 102,522  
; FILING DATE: 04-AUG-1993  
; APPLICATION NUMBER: 980,141  
; FILING DATE: 23-NOV-1992  
; APPLICATION NUMBER: 540,033  
; FILING DATE: 19-JUN-1990  
; APPLICATION NUMBER: 372,162  
; FILING DATE: 27-JUN-1989  
; APPLICATION NUMBER: 267,758  
; FILING DATE: 01-NOV-1988  
; APPLICATION NUMBER: 874,721  
; FILING DATE: 15-JUN-1986  
; APPLICATION NUMBER: 697,987  
; FILING DATE: 04-FEB-1985  
; SEQ ID NO: 1:  
; LENGTH: 4  
; 5496927-1  
Query Match 51.5%; Score 17; DB 6; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2.5e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AVPI 4  
; 1 1 1 1  
; 1 1 1 1  
DB 1 AVPIV 4  
RESULT 12  
5496927-2  
; Patent No. 5496927  
; APPLICANT: KOLB, H.MICHAEL, BURKHART, JOSEPH P.; JUNG, MICHEL J.;  
; GERHART, FRITZ E.; GIROUX, EUGENE L.; NEISES, BERNHARD; SCHIRLIN,  
; DANIEL G.  
; TITLE OF INVENTION: PEPTIDASE INHIBITORS  
; NUMBER OF SEQUENCES: 26  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/248,847  
; FILING DATE: 25-MAY-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 102,522  
; FILING DATE: 04-AUG-1993

APPLICATION NUMBER: 980,141  
FILING DATE: 23-NOV-1992  
APPLICATION NUMBER: 540,033  
FILING DATE: 19-JUN-1990  
APPLICATION NUMBER: 372,162  
FILING DATE: 27-JUN-1989  
APPLICATION NUMBER: 267,758  
FILING DATE: 01-NOV-1988  
APPLICATION NUMBER: 874,721  
FILING DATE: 15-JUN-1986  
APPLICATION NUMBER: 697,987  
FILING DATE: 04-FEB-1985  
SEQ ID NO: 2  
LENGTH: 6  
5496927-2

Query Match 51.5%; Score 17; DB 6; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.5e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVPI 4  
1:1:  
Db 1 ALPV 4

RESULT 13  
US-08-618-693-96  
Sequence 96, Application US/08618693  
Patent No. 5723594  
GENERAL INFORMATION:  
APPLICANT: NEROJSA JANJIC  
APPLICANT: LARRY GOLD  
TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC  
ACID LIGANDS  
NUMBER OF SEQUENCES: 96  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson and Bratschun, L.L.C.  
STREET: 8400 East Prentice Avenue, Suite #200  
CITY: Denver  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 Inch, 1.4 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/618, 693  
FILING DATE: 20 MARCH 1996  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,783  
FILING DATE: 7-JUNE-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER: NEX42/CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 96:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide  
FEATURE:  
OTHER INFORMATION: Xaa at position 5 is a  
OTHER INFORMATION: modified amino acid that could not be identified.  
US-08-618-693-96

Query Match 51.5%; Score 17; DB 1; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.5e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PINAK 7  
1:1:  
Db 3 PIXKK 7

RESULT 14  
US-08-973-124-185  
Sequence 185, Application US/08973124  
Patent No. 6207816  
GENERAL INFORMATION:  
APPLICANT: LARRY GOLD et al.  
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE  
FACTORS  
NUMBER OF SEQUENCES: 304  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Swanson & Bratschun, L.L.C.  
STREET: 8400 E. Prentice Avenue, Suite 200  
CITY: Englewood  
STATE: Colorado  
COUNTRY: USA  
ZIP: 80111  
COMPUTER READABLE FORM:  
MEDIUM TYPE: diskette, 3.5 Inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WordPerfect 6.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,124  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/08014  
FILING DATE: 30-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,423  
FILING DATE: 02-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/458,424  
FILING DATE: 02-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,594  
FILING DATE: 05-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/465,591  
FILING DATE: 05-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,725  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/479,783  
FILING DATE: 07-JUNE-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/618, 693  
FILING DATE: 20-MARCH-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Barry J. Swanson  
REGISTRATION NUMBER: 33,215  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 793-3333  
TELEFAX: (303) 793-3433  
INFORMATION FOR SEQ ID NO: 185:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: Peptide

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;
; FEATURE:
; OTHER INFORMATION: xaa at position 5 is a modif
; OTHER INFORMATION: that could not be identified.
US-08-973-124-185

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Query Match
Best Local Similarity 51.5%; Score 17; DB 3; Length 7;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 3 PIAOK 7
  11 : 1
Db 3 PIXKK 7

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RESULT 15
US-08-991-743C-96
; Sequence 96, Application US/08991743C.
; Patent No. 6229002
; GENERAL INFORMATION:
; APPLICANT: NEROJA JANJIC, LARRY GOLD
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR (PDGF) NUCLEIC
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 1745 Shea Center Drive, Suite 330
; CITY: Highlands Ranch
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80129
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,743C
; FILING DATE: 16-Dec-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/618,693
; FILING DATE: 20-MARCH-1996
; APPLICATION NUMBER: 08/479,783
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/479,725
; FILING DATE: 7-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX66
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 268-0066
; TELEFAX: (303) 268-0065
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FEATURE:
; OTHER INFORMATION: xaa at position 5 is a modified amino acid
; that could not be identified.
; SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-08-991-743C-96

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Query Match
Best Local Similarity 51.5%; Score 17; DB 3; Length 7;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 3 PIAOK 7
  11 : 1
Db 3 PIXKK 7

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Search completed: September 13, 2003, 20:46:41  
Job time : 31 secs